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GenCore version 5.1.6
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July 2, 2004, 10:27:16 ; Search time 3991 Seconds (without alignments) 10871.054 Million cell updates/sec 1 gotgtacccagagagtcctg......gcagaacaaggtaacatgac 1001 6940544 3470272 segs, 21671516995 residues Total number of hits satisfying chosen parameters: US-09-247-874E-2_COPY_8345_9345 OM nucleic - nucleic search, using sw model Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 200000000 gb_btg.*

gb_ov.***

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gb_pt.**

gb_pt.**

gb_vi.**

gb_vi.** GenEmbl:* Title: Perfect score: Sequence: Scoring table: Database : Searched: Run on:

26: em_ro:*
27: em_sts.*
28: em_un:*
29: em_vi:*
30: em_hcg_hum:*
31: em_hcg_num:*
32: em_hcg_other:*
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40: em_hcgo_hum:*
40: em_hcgo_hum:*
40: em_hcgo_hum:*
41: em_htgo_other:*

em_ov:* em_pat:* em_ph:* Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	22711230 22711230 2271230 2	line disease /ertebr ; Homin
SUMMARIES	BD21230 AX052806 AX052806 AX052806 AX067266 BD085956 BD085956 BS1L1B AC079753 BD080413 AC079753 BD080413 BD0804	ALIGNMENTS 9721 bp interstitial 8 ordata; Crani imates; Catar .D. and Whyte interstitial A 2 03-DEC-20
DB		k of 0809; an) an, Cl a, Cl 21) e, F. &
Length		n of risk of 1 GI:3308099 0801.A/2. ens (human) ens: i Metazoa; Ch Eutheria; Pr 1 to 9721 n Giovine,F.S n of risk of
% Query Match		BD271230 Prediction of BD271230 BD271230 BD271230.1 GI BD2002540801 Homo sapiens (Homo Graes) to Buff, G.W., Giore Prediction of Patent: JP 200
Score	1.000000000000000000000000000000000000	
Result No.		RESULT 1 BD271230 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

	RESULT 2 AM052806 AM052806060606060606060606060606060606060606
INTERLEUKIN GENETICS INC COMMENT OS Homos sapiens (human) PN 47 2002540801-A/2 PD 03-DEC-2002 PP 31-MRR-2000 UP 2006608666 PR 10-NRR-2000 UP 2006608666 PR 02-APR-1999 US 09/286108 PI CORDON W DUFF, FRANCESCO SAVERIO DI GIOVINE, MORIA WHYTE PC C12N15/09, A61K31/702 C 01201/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/56, PC C12N15/00, PC A61K37/02 C 12N15/00, PC A61K37/02 CC 11-1B gene Location/Qualifiers FT SOURCE 1. 9721 CC 11-1B gene Location/Qualifiers FT SOURCE 1. 9721 COGANISHERS 1. 9721 COGANISH 1. 9721 COG	Deer Watch Match (1997), 181. DE 6; Length 9721; Deet Local Similarity (1997), 181. DE 6; Length 9721; Deet Local Similarity (1997), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Length 9721; Deet Local Similarity (1998), 181. DE 6. Deet Local Similarity (1998), 181. DE 6. Deet Local Similarity (1998), 181. DE 6. Deet Local Similarity (1998), 181. DEET Conformation (1998), 181. DEET C

ò	301 IGTCATICGCICCCACAITCIGAIGAGCAACGCIITCCCIANTHATHTATHTATHTATHTATHTA 260		
		Best	Query March Best Local Similarity Matches 999; Conser
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ŏ	421 AAAGAGCCTAGTITITAATAGCTATGGAATCAATTTGGACTGGTGTGCTCTCTTT 480	ò	
.8 qc	8765 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTTGAATTTGGACTGGTGTGTCTCTTTT 8824	qu	 8405 AACAGAAAG
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		අ <u>ග</u>	8885 TTTATAAATG
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RESULT 3		ò	661 AGGCTGTGAG
AX067266 LOCUS	AX067266	අු	9005 AGGCTGTGAG
ACCESSION	Sequence 2 from Patent WO0100880. AX067266	ò	721 GAAATATCCT
VERSION KEYWORDS		qu	9065 GAAATATCCT
SOURCE ORGANISM	Homo sapiens (human) Homo sapiens	ò	781 ACAGAAGGAT
	Eukaryota; Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	qa	9125 ACAGAAGGAT
REFERENCE	1 Duff, G.W., Cox, A., Camp, N.J. and di Giovine, F.S.	ò	841 GACTGGTAGT
TITE	Diagnostics and therapeutics for diseases associated with an il-1 inflammatory haplotype	qq	9185 GACTGGTAGT
JOURNAL	Patent: WO 0100880-A 2 04-JAN-2001; Interleukin Genetics, Inc. (US)	à	901 CGCTATGTAC
FEATURES Source	Location/Qualifiers 19721	qq	9245 CGCTATGTAC
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ORIGIN	/db_xref="taxon:9606"	qa	9305 AGGAGAGCA

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Score 997.8; DB 6;
Pred. No. 2e-236;
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Lues, P.J. and Rim, S.

Lud1522586-A 20 20-NOV-2001;

OS Unidentified
PN JP 200152286-A/20
PD 20-NOV-1997 GOD DF 09-NOV-1997 GOD DF 09-NOV-1999 US 09/005923 PI GORDON W DFF, MARKO GIOVAIN, PETER J BARNES, SIMON RIM PC C12N15/09, C12Q1/68, C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Topology: Linear;
CC Methods of diagnosing and treat?
FH Key
FT Source
                                                9005 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTGCTGAGTGCTGCAAGTACCTA 9064
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           661 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTGCTGAGTGCTGCAAGTACCTA 720
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99.7%; Score 997.8; DB 6; Length 9 Best Local Similarity 99.8%; Pred. No. 2e-236; Matches 999; Conservative 0; Mismatches 2; Indels
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DEFINITION
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AUTHORS
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KEYWORDS
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Variants of il-1 beta gene and cd46 gene for diagnosing unexplained recurrent pregnancy loss
Tatent: WO 0222877-A 1 21-MAR-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; DANA-FARBER CANCER INSTITUTE, INC. (US)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                           DNA
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                                                                       AX469435 9721 bp
Sequence 1 from Patent W00222877.
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Clark, B.D., Collins, K.L., Gandy, M.S., Webb, A.C. and Auron, P.E.
Genomic sequence for human prointerleukin 1 beta: possible
evolution from a reverse transcribed prointerleukin 1 alpha gene
Nucleic Acids Res. 14 (20), 7897-7914 (1986)

Data Kindly reviewed (13-MAY-1988) by Clark B.D.
1.9721
1.9721
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7.mol_type="genomic DNa"
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3490654

source

DNA library"

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misc_feature misc_feature

576. .1581 note="TATA-box like sequence"

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo

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AUTHORS
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Anote="pot. viral enhancer core sequence"
2458. 2458

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2466. 2527

'number=2

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prim_transcript

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CAAT_signal CAAT_signal TATA_signal

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Join (2481 . .2527,3092 . .3143,5125 . .5326,5874 . .6038,7275 . .7405,8127 . .8339)
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5125. .5326
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interleukin 1 beta.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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linear

DNA

9721 bp DN. Human gene for prointerleukin 1 beta. X04500

LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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RESULT HSIL1B

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780

9124

9184

9244

900

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Enkaryota Metazoa: Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 1747)

Ridear, M. J., Armel, T.Z., Carrington, D.P., Ozuna, M., Kuldanek, S.A., Rajkumar, N.R., Toth, E.J., Yi,Q. and Nickerson, D.A.

Rajkumar, N.R., Toth, E.J., Yi,Q. and Nickerson, D.A.

Direct Submission

Submitted (29-UUL-2002) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA

To cite this work please use: SeattleSNPs. NHLBI HL66682 Program for Genomic Applications UW-FRCRC, Seattle, WA (URL: Location) Qualifiers

Increin. 17447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY137079 17447 bp DNA linear PRI 05-AUG-2002
Homo sapiens interleukin 1, beta (IL1B) gene, complete cds.
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                                 9065 GAAATATCCTIGGCCACCGAAGACTATCCTCCTCACCCATCCCCTTATTTCGTTGTTCA
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Best Local Similarity 99.7%; Score 997.8; DB 9; Length 9721;
Best Local Similarity 99.8%; Pred. No. 2e-236;
Matches 999; Conservative 0; Mismatches 2; Indels 0;
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/note="pot.viral enhancer core sequence"
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/note="pot.viral enhancer core sequence"
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/number=5
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/number=5
6205. .6212
/note="inverted repeat A"
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/note="pot polyA signal"
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39244027 /rpt_family="MIR" /rpt_type=dispersed 4006_Ype=dispersed /gene="ILIB" /frequency="0.15" /replace="a" /rpt_family="1"	/rpt_treats	/gene="ILIB" /frequency="0.99" /replace="" 4325ae="ILIB" /gene="ILIB" /replace="t"	4392 /gene="ILIB" /requency="0.21" /replace="c" 4505 /gene="ILIB" /frequency="0.01" /replace="t"	/rpt_rype=dispersed 5200— fane="LilB" /frequency="0.34" /replace="a" 5277 /requency="0.18" /replace="t" 5916 /replace="t" /gene="LilB" /gene="LilB" /frequency="0.03"	/replace="t" 6293" /gans="ILIB" /frequency="0.01" /replace="c" /gans="ILIB" /frequency="0.21" /replace="a"	/ frequency="0.01" / frequency="0.01" / frequency="0.01" / gene="ILIB" / frequency="0.21" / frequency="0.21" / frequency="0.23" / frequency="0.23" / frequency="0.23" / frequency="0.15" / frequency="0.15" / frequency="0.15"
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Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jun 6, 2001 Lhis sequence version replaced gi:14029079.
                                                                                                                                                                                                                         AC079753 154214 bp DNA linear PRI 01-MAR-2002
Homo sapiens BAC clone RP11-67L14 from 2, complete sequence.
AC079753
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Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Submitted (03-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 61108, USA
                                                                                                                                                                                                                                                                                                                    Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Missouri 63108,
                                                                                 8634 GTTGAGCZAGCGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCCACAAGTCC
                     GGGAGTCAGGACTGGTAGTAACAGCTACCA-TGATTTATCTATCAATGCACCAAACATCT
                                                              891 GITGAGCAAGCGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCACAAGTCC
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4444 Forest Park Parkway, St.
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                                                                                                                        CTCCTCAGATAGGAGGCAGCTAGTTATAAGCAG-AACAAGGTAACATGAC
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Andrews, S., Cotton, M., Doebber, A. and Rose, C.
The sequence of Homo sapiens BAC clone RP11-67L14
Unpublished (2001)
3 (bases 1 to 154214)
Waterston, R.H.
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Submitted (09-JAN-2002) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
7 (Dases 1 to 154214)
Waterston,R.
                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 154214)
Sulston,J.B. and Waterston,R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Submitted (06-JUN-2001) Genome
University School of Medicine,
MO 63108, USA
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Waterston, R.H.
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85.8%; Score 858.8; DB 9;
Best Local Similarity 95.2%; Pred. No. 5.5e-202;
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7275
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Louis,

repeat_region

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NOTICE: This sequence may not represent the entire insert of this cone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Morbherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5:1:-8 The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the right is RP11-725V3. Actual start of this clone is at base position 1 of RP11-67L14; actual end is at base position 154214 of RP11-67L14.

There are polymorphic base differences in the overlap between RP11-67L14

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4 and RP11-725J3.
Location/Qualifiers
1. .154214
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Length 154214;

85.6%; Score 857.2; DB 9; 95.1%; Pred. No. 1.3e-201;

Query Match Best Local Similarity

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15744. .16120
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DEFINITION Novel molecules of the Tango-77 related protein family and uses thereof. ACCESSION BD080414. G1:22626017 EB080414.1 G1:226260	Query Match 84.8%; Score 848.6; DB 6; Length 175373; Best Local Similarity 95.8%; press No. 1.76-199; deges 37; conservative 0; Mismatches 24; Indels 19; daps 9; QV 1 GCTGTACCCAGAGACTCCTGTGGACTCCAACCCTAGGGCTGGCAGAAGGG 16.209 GCTGTACCCAGAGACTCCTGTGGACTCCAACCCTAGGGCTGGCAGAAGGG 136.19 136.10
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QY 121 CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 180 Db 6908 CAACTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 6967 QY 181 CTGTCTCTTTCAGGGCCAATCCCCAGCCCTTTTGTTGAGCCAGGCCTCTCTCACCTCTC 240 Db 6968 CTCTCTCTTTTCAGGGCCAATCCCCAGCCCTTTTGTTGAGCCAGGCCTCTCTCACCTCTC 240 CTCTCTCCTTTAAGAGCCCAATCCCCAGCCCTTTTGTTGAGCCAGGCCTCTCTCACCTCTC 7027 QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACCACGGCCAATTTGTTCTAAGAAACCCTC 300 Db 7028 CTACTCACTTAAAGCCCGCCTGACAGAAACCAGGCCACATTTGTTCTTAAGAAACCCTC 7087 QY 301 TGTCATTGGTTCCCACATTCGATGAAACCACCCCACATTTGTTCTAAAGAAACCCTC 7087 QY 301 TGTCATTTGGTTCCCACATTCGATGAAACCACCCTATTTAGTTTATTTA	7088 TGTCATTCGCTCCCACATTCTGATGAGCAACCGCTTCCCTATTTATT		Db 7447 AACAGGCTGTGAGATTCTTGGGGACTAAAGCCCACCTCCTTGCTGAGTGTTTTTTTT	RESULT 11 HUMILIB LOCUS DEFINITION Human interleukin 1-beta (ILIB) gene, complete cds. ACCESSION MIS640. REXION MIS640. REXION MIS640. ALU repeat; interleukin 1-beta. CRGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) Advaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
13 5 13 6 13 4	135 135 135	Qy 829 GCAGGAGTCAGGACTGGTAGTAACAGCTACCA-TGATTTATCTATCATGCACCAAACA 887 Db 135374 GCAGGAGTCAGGACTGATTAACAGCTACCATTGATTTATCTATC	RESULT 10 AX774856 AX774856 DETINITION Sequence 172 from Patent W003038129. AX774856.1 G1:32486372 AX774856 AX77486 AX77486 AX77486 AX7748	Query Match 83.4%; Score 834.6; DB 6; Length 7824; Best Local Similarity 94.2%; Pred. No. 5.5e-196; Indels 15; Gaps 8; Qy 1 GCTGTACCCAGAGATCCTGTGCTGATGACTCAATCCTAGGCTGCAGAAAGG 60 Db 6788 GTTTTACCCAGAGATCTGTGTGATTACCTGATTCCTAGGGTGGCAGAAAGG 647 Qy 61 AACAGAAAGGTTTTGAGTAACGGTAAACCTGGACTTCTGTTGTCTACACCAAAAGG 6847 Db 6848 AACAGAAAGGTTTTTGAGTAACGGCTATAACCTGGACTTTCCTGTTGTCTACACCAATGCC 120 Db 6848 AACAGAAAGGTTTTTGAGTAACGGCTATAAGCCTGGACTTTCCTGTTGTCTACACCAATGCC 6907

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                                                                                                                                                                                              Length 7824;
                                                                                                                    /number=7
region 7280. 7379
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242 bp upstream of HindIII site; chromosome 2q13-q21.
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6570. .s6782
/gene="ILIB"
                                                                                                                                                                                              Score 834.6; DB 9;
Pred. No. 5.5e-196;
0; Mismatches 44;
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ilarity 94.2%;
Conservative 0
                number=6
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Matches 956; (
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                                                                                                                                                                                                                                                                                                                                                                                                         "note="ILlb intron A; G00-120-094"
join(924. .970,1536. .1587,3576. .3777,4323. .4487,5723. .5853,
5570. .6783)
gene="ILlB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGGIQLRISDHHYSKGFRQAASVVVAMDKLEKCLVPCPQTFQENDLSFFFFFFFFFEEP
IFPOTWDNEAYVHDAPVRSINCTLRDSQQKSLVMSGPYELKALHLQGQDMEQQVVFSM
SFVQGESNDKI PVALGLKEKNLYLSCVLKDDKPTLQLESVDPKNYPKKKMEKRFVFN
KIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGQDITDFTMQFVSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="GDB:G00-120-094"
translation="MAEVPELASEMMAYYSGNEDDLFFEADGPKQMKCSFQDLDLCPL
                                                                                                                 Bensi, G.
Direct Submission
Submitted (26-MAY-1987) G. Bensi, Sclavo Research Center, Siena,
   Raugei, G., Palla, E., Carinci, V., Tornese Buonamassa, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="interleukin-1 beta, (first expressed exon); 300-120-094"
                                                                                                                                                                                                                                                                                                                         374. .7380
/gene="Lilb"
/hote="Lilb mRNA and introns; G00-120-094"
446. 908
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/gene="ILLB"
/note="ILLD intron C; G00-120-094"
3110. .3429
/note="Allu repeat copy A; G00-120-094"
3576. .3777
/gene="ILLB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .536. .1587
/gene="illB"
/note="interleukin-1 beta; G00-120-094"
/number=3
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5723. .5853
/gene="ILIB"
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gene="ILIB"
note="ILIB intron D; G00-120-094"
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gene="ILIB"
note="ILID intron B; G00-120-094"
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product="interleukin 1-beta"
protein_id="AAA74137.1"
db_xref="GI:386816"
                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"
/map="2q13-q21"
/clone="Lambda-hilb[4,8]"
                                                                                                                                                                           Original source text: Human DNA.
Location/Qualifiers
1. 7824
                        Human interleukin-1 beta gene
Gene 52 (1), 95-101 (1987)
87248099
                                                                                                                                                                                                                                                                                   /clone="Lambda
374. .7380
/gene="IL1B"
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/gene="IL1B"
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gene="IL1B"
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           Bensi, G., Rand Melli, M
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human STS CHLC.UTR_00699_X04500.P37183 clone UTR_00699_X04500,
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( Dases 1 to 614)

Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.H.
Cooperative Human Linkage Center
Unpublished (1995)
                   120394 GCTGAGTGCTGCAAAGTACCTAAAAATATCCTTGGCCACCGAAGACTATCCTCCTCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120334 ATCCCCTTTATTTCTGTTGTTCAACAGAAAGGATATTCAGTGCACATCTGGAACAGGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120214 TGCACCAAACATCTGTTGAGCAAGCGCTATGTACTAGGAGCTGGGAGTACAGAGAGA
 TGTGCTCTCTTTAAATCAAGTCCTTTAATTAACACTGAAAATATATAAAGCTCAGATTA-T
                                                                                                   120634 IGIGCTCTTTTAAATCAIGTCCTTTAATTACGACTGAAAATATATCTGCTCCGATCATT
                                                                                                                                                                           120574 TTAAGTGGGAATATTTATGAAATTACCAAATATCATACTGTTCAATGATTCTGAAATAAA
                                                                                                                                                                                                                                                    120514 CTTCACTGAACAAAAAAAAAAGGTCTTTCCTGATCATTGACTTGTCTTGGATTTTGACACT
                                                                                                                                                                                                                                                                                                             120454 GAACAGTAAAGACACCCAGGGCTGTGAGAGTTCTTGGGGGACTAAAGCCCCACTCCTCATT
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                                                                                                                                             528 TTAAATGGGAATATTTAT-AAATGAGCAAATATGATACTGTTCAATGTTCTGAAATAAA
                                                                                                                                                                                                                  CTTCACTGAAGAAAAAAAAAAAGGGTCTCCTGATCATTGACTGTCTGGATTGACACT
                                                                                                                                                                                                                                                                                        647 G-ACAGTAAGCAAAC---AGGCTGTGAGAGTTCTTGGG---ACTAAGCCCACTCCTCATT
                                                                                                                                                                                                                                                                                                                                                               700. GCTGAGTGCTGC-AAGTACCTAGAAATATCCTTGGCCACCGAAGACTATCCTCCTCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCCCCTTTATTTC-GTTGTTCAACAGAAGGATATTCAGTGCACATCTGGAACAGGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          818 GCTGAAGCACTGCAGGAGTCAGGACTGGTAGTAACAGCTACCA-TGATTTATCTATCAA
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Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3368
Fax: (319) 356-3347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STS; STS sequence; primer; sequence tagged site.
Homo sapiens (human)
Homo sapiens
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Primer B: CTTGCCCCCTTTGAATAAT
STS size: 229
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Contact: Dr. Jeffrey C. Murray
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152331)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel molecules of the Tango-77 related protein family and uses Patent: JP 2001512002-A 5 21-AUG-2001;
MILLENIUM PHARMACEUTICALS INC
OS Home. sapiens (human)
PN JP 2001512002-A/5
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                 120933 ATGNAANTCAGCTCTGGTTCTTCAGGGACAATCCCCAGCCCTTTTGTTGAGCCAGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGTTGAGCAAGCGCTATGTACTAGGAGCTGGGAGTACAGATGAGAACAGTCACAAG
                                                                                                     TCTCACCTCTCCTACTCACTTAAAGCACGCCTGACAGAAACCACGGCCACATTTGGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTATTTGTTTGTTTTGTTTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAA
GCAGGGAGTCAGGACTGGTAGTAACAGCTACCA-TGATTTATCTATCAATGCACCAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 TCTCACCTCTCCTACTCACTTAAAGCCCGCCTGACAGAAACCACGGCCACATTTGGTTCT
                                                                                                                                         AGGACAGTCACCTCTCTCAGGGCCAATCCCCAGCCCTTTTGTTGAGCCAGGCCTC
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03-AUG-1998 JP 2000505182
04-AUG-1997 US 60/054646,02-JUL-1998 US
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llarity 90.9%; Pred. No. 7.2e-140;
Conservative 0; Mismatches 62;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                          BD080413.1 GI:22626016
JP 2001512002-A/5.
Homo sapiens (human)
Homo sapiens
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PC C12Q1/68,C07F
C12Q1/02,
PC G01N33/15,G01
7088,A61K38/00,
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/organism="Homo sapiens"
/mol_type="mRNA"
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BC008678.1 GI:14250476
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Homo sapiens (human)
Homo sapiens
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Location/Qualifiers
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            seconds at 94 degrees C seconds at 55 degrees C seconds at 72 degrees C
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each 1.5 pmole
each 200 uM
0.3 units
10 ul
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Pred. No. 2.9e-139;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                 30
15
27
6
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180. .200
complement (389. .408)
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Total Vol:
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50mM
10mM
                    denature:
annealing:
extension:
PCR cycles:
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KCl:
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Best Local Similarity 99.7%;
Matches 607; Conservative (
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PCR Profile:
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N. K.,
Hopkins, R.F., Jordan, H., Morce, T., Mans, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M., B., Bonaldo, M.F., Casavanch, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bonaste, B.H., McZhards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Malak, S. Soderstein, E.J., Luk, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse coDNA sequences.
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Email: ggapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center BCN-HGSc.
Center code: BCN-HGSc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunazatne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27894305.
Location/Qualifiers
1522 bp mRNA linear PRI 04-OCT-2003 IMAGE:3875593), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1522)
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Direct Submission
Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Submitted (25-MAY-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, MD 20892-2590,
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
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DGGIOLRISDHHYSKGFRQAASVVVAMDKLRKMLVPCPQTPQBNDLSTFFPFIFEEP
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Mammalia, Eutheria, Primates, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases I to 1473)

Kotenko, S. V., Bulenkov, M.T., Veiko, V.P., Epishin, S.M.,
Lomakin, I.B., Emel'yanov, A.V., Kozlov, A.P., Konusova, V.G.,
Kotov, A.Y., Kurbatova, T.V., Reshernikov, V.L., Simbirtsev, A.S.,
Ketlinskii, S.A. and Vinnetskii, Y.P.
Cloning of the cDNA coding for human prointerleukin-1 alpha and
Dokl. Akad. Nauk SSSR 309 (4), 1005-1008 (1989)
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                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="prointerleukin-1 beta"
                                                                                                                                                                                         prointerleukin 1; prointerleukin 1 beta.
Homo sapiens (human)
Homo sapiens
                                                                                                            mRNA
                                                                                                          HSPROIIB
Human mRNA for prointerleukin 1 beta.
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|organism="Homo sapiens"
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llarity 99.3%; Pred. No. 6.7e-136;
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Novel methods and nucleic acids for diagnosing and treating disorders associated with high levels of interleukin lbeta, especially inflammatory diseases.

(INTE-) INTERLEUKIN GENETICS INC. Di Giovine FS;

WPI; 2000-558192/51.

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                               The present sequence is that of human interleukin-1 beta (IL-IB) allele 2 (+6912), which is a form of the IL-IB gene that contains guanine at position 46912, IL-IB allele 1 (+6912) has cytosine at this position (see position 46912 iL-IB allele 1 (+6912) has cytosine at this position (see ALASO174). The invention is based on the identification of this novel allele at marker +6912 of the IL-IB gene. The C to G transition occurs within the 3 untranslated region of the IL-IB gene and results in an increased level of IL-IB protein. Individuals homozygous for the IL-IB allele 2 (+6912) accumulate approximately 4 times more immunoreactive IL-IB protein than homozygotes for IL-IB allele 2 (+6912), and thereby are provided for detecting IL-IB allele 2 (+6912), and thereby disorders, especially coronary artery disease, osteoporosis, nephropathy in diabetes mellitus, alopecia areata, Graves disease, systemic lupus critinopathy, periodontal disease, ulverative colitis, diabetic retinopathy, periodontal disease, juvenile chronic arthritis, psoriasis, insulin dependent diabetes, asthma, chronic inflammatory lung disease, juvenile chronic arthritis, claimed). Identification of the IL-IB allele 2 (+6912) and its involvement in IL-IB overproduction also eables screening assays for involvement in IL-IB overproduction also eables screening assays for involvement in IL-IB overproduction also eables screening assays for involvement in IL-IB also eables screening assays for involvement in IL-IB also eables screening assays for involvement in IL-IB also eables screening assays for involvement in IL-IB also eables screening assays for involvement in IL-IB also eables screening assays for involvement in IL-IB also eables screening assays for involvement in IL-IB also eables screening assays for involvement in IL-IB also eables screening assays for involvement in IL-IB also eables screening assays for involvement in IL-IB also eables screening assays for involvement in IL-IB also eables screening assays for involvement in IL-IB and its 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identifying IL-1B antagonists that can be used to treat conditions associated with IL-1B allele 2 (+6912). Transgenic animals are also claimed, and can be used to identify IL-1B agonists and antagonists, to confirm the safety and efficacy of candidate therapeutics
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llarity 99.9%; Pred. No. 3.1e-235;
Conservative 0; Mismatches 1; Indels 0;
Claim 34; Fig 2; 74pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes genotyping a nucleic acid sample from a subject to determine at least one allele of an interleukin-1 [IL-1] proinflammatory haplotype. A method has also bee described for determining a subject's susceptibility to developing chronic obstructive airway disease (COAD) or for predicting the rapidity or ultimate progression of a COAD in the subject by: (a) obtaining a nucleic acid sample from the subject, and (b) detecting at least one allele of an IL-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genotyping nucleic acid samples for interleukin-1 (IL-1) proinflammatory haplotype alleles, useful for predicting susceptibility to developing chronic obstructive airway disease.
                                                                      9005 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTGCTGAGTGCTGCAGTACTA
                                                                                                                                                   GAAATATCCTTGGCCACCGAAGACTATCCTCCTCACCATCCCTTTATTTCGTTGTTCA
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chronic obstructive airway disease, chronic bronchitis, emphysema,
asthma, chronic bronchiolitis, proinflammatory haplotype; ss.
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98US-00005923.
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proinflammatory haplotype in the sample, where detection of at least one of these alleles indicates that the patient has an increased susceptibility to developing COAD. The method is useful for determining the susceptibility of subjects to developing chronic obstructive airway disease or for predicting the rapidity or ultimate progression of chronic obstructive airway disease (COAD). COAD can be asthma, emphysema, chronic bronchicits. The method provides for early identification of chronic obstructive airway disease (COAD), facilitating administration of appropriate treatment at the earliest stage, thereby increasing the probability of a positive outcome. The present sequence represents the human IL-1B gene
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Best Local Similarity 99.87
Marches 999; Conservative
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Human; ds; gene; interleukin-1B; IL-1B; chromosome 2q13; nephropathy; inflammatory disease; Systemic Inflammatory Response; SIRS; athritis; acute joint inflammation; opthalmopathy; uvenile chronic arthritis; acute joint inflammation; opthalmopathy; uvenile chronic arthritis; asthma; bronchial asthma; pulmonary disease; chronic obstructive airways disease; cardiovascular disease; thyroditis; atheoric consts; autonimmune carditis; cardiowypathy; ulcerative colitis; ardiac cell disfunction; aortic smooth muscle cell activation; trauma; ardiac cell apoptosis; gastrointestinal inflammation; cerebral trauma; winflammatory bowel disease; HIV infection; coronary artery lesion; Kawasaki's syndrome; cervical lymphadenopathy; diabetic nephropathy; diomerulonephritis; diabetic retinopathy; diabetic nephropathy; of steporosis; bone loss; otitis media; pancreatitis; periodontal disease; winnary tract infection; chronic prostatitis; immunological disease; chronic sinusitis; immunological disease; chronic prostatitis; immunological disease; chronic prostatitis; immunological disease; chronic property areas alopecia areata; drave's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for determining whether a subject has or is predisposed to developing a disease or condition that is associated with an IL-1 inflammatory haplotype. The method involves detecting at least one allele of the haplotype, where the presence of the allele indicates that the subject is predisposed to the development or has the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                urinary tract infection; chronic prostatitis; immunological disorder; chronic pelvic pain syndrome; alopecia areata; Grave's disease; thyroid disease; goiter; struma lymphomatosa; sleep disorder; neoplasia; chronic fatigue syndrome; obesity; infectious disease; Leishmaniasis; Leprosy; myocardial disfunction; breast cancer; organ transplant; Hodgkin's disease; hormonal regulation; fertility; septicaemia.
GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAACATCTGTTGAGCAAG
                                       GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAACATCTGTTGAGCAAG
                                                                                                                     CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCACAAGTCCCTCCTCAGAT
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                                                                                                                                                                                              961 AGGAGAGCAGCTAGTTATAAGCAGAACAAGGTAACATGAC 1001
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99US-00345217.
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30-JUN-1999;
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disease or condition. The invention allows the determination of an individual's likelihood for developing a particular disease or condition associated with interleukin 1 (IL-1) polymorphisms without necessarily determining or characterising the causative genetic variation. Diseases such as inflammatory disease e.g. acute joint inflammatory Response (SIRS), Alzheimer's disease, arthritis e.g. acute joint inflammation, juvenile chronic arthritis; asthma e.g. bronchial asthma, chronic obstructive airways disease; cardicovascular diseases e.g atherosclerosis, autoimmune carditis; cardicomyopathy and cardiac cell disfunction e.g. acutic smooth inflammations e.g. inflammatory bowel disease, ulcerative colitis; HIV inflammations e.g. inflammatory bowel disease, ulcerative colitis; HIV inflammations, nephropathy coronary artery lesions; nephropathse e.g. diabetic nephropathy, coronary cartery lesions; nephropathse e.g. diabetic nephropathy, coronary corphalmopathy; osteoporosis e.g. diabetic nephropathy, coronary cophalmopathy; osteoporosis e.g. diabetic nephropathy, coronary coronic simusitis; buyroditis e.g. chronic lung disease; chronic simusitis; buyroditis e.g. chronic lung disease; chronic simusitis; thyroditis e.g. chronic lung disease; chronic simusitis; trauma e.g. carcers e.g. alopecia areato, Graves disease; chronic fatigue syndrome; obesity; infectious diseases e.g. teprosy infectious diseases e.g. teprosy infectious diseases e.g. teprosy corphasias e.g breast cancer, Hodgkin's disease; hermonal regulation e.g. fertility, septicaemia; organ transplants. This allows for a more customised approach to preventing the onset or progression of the disease or condition. The corpicion senders are necessated to preventing the onset or progression of the disease or condition. The preventing the sequence of the human interleukin-18 gene corporated and condition. The preventing the sequence of the human interleukin-18 gene corporations.
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Sequence 9721 BP; 2661 A; 2329 C; 2121 G; 2608 T; 0 U; 2 Other;

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99.7%; Score 997.8; DB 2; Length 9721; 99.8%; Pred. No. 7.8e-235; vative 0; Mismatches 2; Indels 0; Gaps	GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAAGG 60	GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 8404	AACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC 120	AACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACAATGCC 8464	CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 180	CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 8524	CCTITCAGGGCCAATCCCCAGCCCTTIGITGAGCCAGGCCTCTCTCACTCTC 240	CTCTCTCTTTCAGGGCCAATCCCCAGCCCTTTTGTTGAGCCAGGCCTCTCTCT	CTACTCACTTAAAGCCCGCCTGACAGAAACCACGACGCCACATTTGGTTCTAAGAAACCCTC 300	CTACTCACTTAAAGCCCGCCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCTC 8644	INGRCATICGCICCCACATICIGAIGAGCAACCGCIICCCIAITIAITIAITIAITIGII 360	TGTCATTCGCTCCCACATTCTGATGAGCAACCGCTTCCCTATTTATT	GITIGITITGATICATIGGICIPATITIATICAAAGGGGGCAAGAAGTAGCAGIGICIGIA 420	GITTCITTTCATTCATTCGTCTAATTATTCAAGGGGGGCAAGAGTAGCAGTGTCTCTA 8764	AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCAAT	AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTTGGACTGGTGTGCTCTTTT 8824	AAATCAAGTCCTTTAATTAACACTGAAAATATATAAAGCTCAGATTATTTAAATGGGAATA 540	AAATCAAGTCCTTTAATTAAGACTGAAAATATAAGCTCAGATTATTTAAATGGGAATA 8884	TTTATAAATGAGCAAATATGATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 600
넏	GCTGTACC	GCTGTACC	AACAGAAA	AACAGAAA	CAACTGCC	CAACTGCC	CTCTCTCC	CTCTCTCC	CTACTCAC	CTACTCAC	TGTCATTC	TGTCATTC	GTTTGTTT	GTTTGTT	AAAGAGCO	AAAGAGCC	AAATCAAG	AAATCAAG	TTTATAA
Query Match Best Local Sir Matches 999;	r	8345	61	8405	121	8465	181	8525	241	8585	301	8645	361	8705	421	8765	481	8825	541
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Disclosure; Page 673-675; 1343pp; English.

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                                                                 901 CGCTATGTACTAGGAGCTGGGAGTACAGAGGAGGACAGTCACAAGTCCCTCAGAT
                                                                                                                            9065 GAAATATCCTTGGCCACGGAGGACTATCCTCCTCACCCATCCCCTTTATTTCGTTGTTCA
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                                                 601 AAAAAAAAGGGTCTCTCTGATCATTGACTGTCTGGATTGACACTGACAGTAAGCAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human adenosine receptor related polynucleotide SEQ ID NO:2512.
                                                                                                                                                                                                                                                                                                                                                                                                                                   961 AGGAGAGCAGCTAGTTATAAGCAGAACAAGGTAACATGAC 1001
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             The present invention describes a new composition comprising an antisense oligonal eacide (NN) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antionflammacory, antiallergie, and/or antiastimatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired alrways, including lung disease and diseases whose secondary effects affilict the lungs of a subject. They can be used for treating effects affilict the lungs of a subject. They can be used for treating of e.g. ischaemic conditions, pulmonary visconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive could fibrosis, pulmonary hypertension, emphysema, chronic obstructive contensors and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the reduces and prostate cancer. The A-containing ONS break down with the release of decoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA12313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present content on the previously named sequences. SEQ ID No:11 to 1680 (AAA3233 to AAA3392) are specifically claimed ONE from the present invention, on the the invention of one match in the disclosure of the present invention do not match in the interpretation of the present invention of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coronary artery disease; osteoporosis; nephropathy; alopecia areata; draves disease; systemic lupus erythematosus; lichen sclerosis; ulcerative collisis; diabetic retinopathy; periodontal disease; juvenile chronic arthritis; psoriasis; insulin dependent diabetes; asthma; lung fibrosis; chronic inflammatory liver disease; rheumatory; osteopathic; dermatological; immunosupressive; antiinflammatory; osteopathic; dermatological; immunosupressive; antidiabetic; antithyroid; antiarbhritic; antitheumatic; antiasthmatic; antipsoriatic; hepatotropic; antiulcer; diagnosis; therapy; ds.
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                                                                                                                9005 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTGCTGAGTGCTGCAAGTACCTA
601 AAAAAAAAAGGGTCTCTCCTGATCATTGACTGTCTGGATTGACACTGACAGTAAGCAAAC
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                                                                                    661 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTGCTGAGTGCTGCAAGTACCTA
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/note= "IL-1B allele 1 (+6912)"
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9065 GAAATATCCTTGGCCACCGAAGACTATCCTCCTCACCCATCCCCTTATTTCGTTGTTCA 9124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatio; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasconstriction; asthma, RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hyperension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                     9005 AGGCTGTGAGAGTTCTTGGGACTAGCCCACTCCTCATTGCTGAGTGCTGCAGTACCTA
                                                       AAAAAAAAAAAGGGTCTCTCCTGATCATTGACTGTCTGGGATTGACACTGACAGTAAGCAAA
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(NYCE/) NYCE J W.
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                                                                The present sequence is that of human interleukin-1 beta (IL-IB) allele 1 (+6912), which is a form of the IL-IB gene that contains cytosine at (+6912), which is a form of the IL-IB gene that contains cytosine at (+6912). IL-IB allele 2 (+6912) has guanine at this position (see AAASO175). The invention is based on the identification of this novel allele at marker +6912 of the IL-IB gene and results in an increased level of IL-IB protein. Individuals homozygous for the IL-IB content than homozygotes for IL-IB allele 2 (+6912). Methods and kits are provided for detecting IL-IB allele 2 (+6912), or an allele in a reprovided for detecting IL-IB allele 2 (+6912), or an allele in a reprovided for detecting IL-IB allele 2 (+6912), and thereby a patient's susceptibility to developing inflammatory of disorders, especially coronary areata, Graves disease, systemic lupus in diabetes mellitus, alopecia areata, Graves disease, systemic lupus criming a patient's alopecia areata, Graves disease, systemic lupus crimina dependent disease, ulcerative colitis, diabetic criminatory lung disease, ulcerative colitis, diabetic criminatory lung disease, lung fibrosis, and rheumatory lord carthritis (claimed). Identification of the IL-IB allele 2 (+6912) and its involvement in IL-IB nuckeroduction also eables screening assays for involvement in IL-IB allele 2 (+6912). Transgenic animals are also colaimed, and can be used to identify IL-IB agonists and antagonists, or confirm the safety and efficacy of candidate therapeutics
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lmmunosuppressive; dermatological; antimicrobial; antiarthritic;
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Query Match 99.7%; Score 997.8; DB 5; Best Local Similarity 99.8%; Pred. No. 7.8e-235; Matches 999; Conservative 0; Mismatches 2;
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9125 ACAGAAGGATATTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG 9184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing or determining susceptibility to developing restenosis involves detecting restenosis associated allele in a nucleic acid sample.
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lained recurrent pregnancy loss; immunologic reproductive failure; prointerleukin-lbeta; IL-lbeta; human; ds.

(first entry)

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Evaluating risk of unexplained recurrent pregnancy loss in a subject, testing presence of a variant in interleukin-1 beta promoter region and/or in CD46 gene intron 1 region in a sample obtained from the subject.
                                              Human prointerleukin-1 beta (IL-1 beta) gene.
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                                                                                                           The invention relates to a method for evaluating and treating risk of unexplained recurrent pregnancy loss (URPL) in a subject suspected of having immunologic reproductive failure. The method involves testing a sample obtained from the subject for the presence of a variant in the human interleukin-lbeta (IL-lbeta) promoter region, and/or a variant in the CMS gene intron 1 region, where the presence of the variant in indicates an elevated risk of developing recurrent pregnancy loss. The present sequence is human prointerleukin-1 beta (IL-1 beta) gene
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Example 2 and 3; Page 51-54; 57pp; English
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Nyce JW, Miller S,

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonuclectide antisense to the initiation codon, coding region, 5 'or 3' end genomic flanking regions, 5 'and 3' intron-exon junctions, or regions within 2-10 nuclectides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antialeregic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ungiunione or lung surfactant in a subject stissue, or treating bronchoconstriction, lung auffactant in a subject stissue, or treating bronchoconstriction, lung surfactant in a subject stissue, or treating bronchoconstriction.

Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WiPo at the printed specification, but was obtained in electronic format directly from WiPo

rnarmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 11881; 872pp; English

Human interleukin-1 nucleic acid. 9721 (first entry) ABZ96639 standard; DNA; 17-OCT-2003 ABZ96639; RESULT 10
ABZ96639
ID ABZ96
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Human, antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy, antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

WO200285308-A2. 31-OCT-2002

24-APR-2001; 2001US-0286137P. 23-APR-2002; 2002WO-US013135

(EPIG-) EPIGENESIS PHARM INC

AAATCAAGTCCTTTAATTAACACTGAAAATATATAAGCTCAGATTATTAAATGGGAATA 540

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8404 8644 8464 8524 8584 8704 8764 120 180 240 300 360 420 cracicacitraaagcccgccrgacagaaaccacgccacarrirggrictaagaaacccrc AAAGAGCCTAGTTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTCTTT 8345 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG CAACTGCCTTAAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG CTCTCTCCTTTCAGGGCCAATCCCCAGCCCTTTTGTTGAGCCAGGCCTCTCTCACCTCTC GTTTGTTTTGATTCATTGCTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG **AACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC** CTCTCTCTTTCAGGGCCAATCCCCAGCCCTTTTGTTGAGCCAGGCCTCTCTCACCTCTC CTACTCACTTAAAGCCCGCCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCTC GITTGITTTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other; ö 99.7%; Score 997.8; DB 7; Length 9721; llarity 99.8%; Pred. No. 7.8e-235; Conservative 0; Mismatches 2; Indels 0; Best Local Similarity Matches 999; Conser 61 121 181 8525 8585 8645 8705 421 Query Match 8465 241 301 361 g ò g ò g ò ద 8 엄 8 ద à 원 à ద

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reagent comprising an interactive sensor pair. The detection reagent is useful for monitoring molecular assembly events to permit the dissection of genetic and non-genetic influences on a particular biological activity. The method is useful for linking genetic variations to molecular and physiological events, drug screening, diagnostics, therapy selection and dosing, patient monitoring or environmental safety. The interactive sensor pairs may be used to screen for and identify novel agonists and antagonists or other molecules that modulate a biological activity. The method is also useful for selecting an appropriate targeted therapeutic for a subject having an infection, including viral, bacterial or fungal infection. It is also used in gene therapy. The present sequence is human interleukin-I (IL-1) allelic gene. This sequence is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781 ACAGAAGGATATTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG 840
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                                                                                                                                                                                                                        Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                    Length 9721;
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Pred. No. 7.8e-235;
0; Mismatches 2;
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Best Local Similarity 99.8<sup>7</sup>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drug screening; fungicide; gene therapy; antibacterial; infection; virucide; human; interleukin-1; IL-1; gene; ds.
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9185 GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAACATCTGTTGAGCAAG
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                                                                                                                                                                                                                                                            Barly onset; progression; ageing-related condition; BOA; allele;
interleukin; (IL)-1; pattern 1; pattern 2; pattern 3; osteoporosis;
osteoarthritis; wrinkled skin; age-related cancer; lifestyle; exercise;
diet; nutraceutical; ds.
                               GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAACATCTGTTGAGCAAG
                                                                       CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAAAGAGTCACAAAGTCCCTCACAGAT
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                                                                                                                                                                                                                                              Interleukin-1B nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                        (INTE-) INTERLEUKIN GENETICS INC.
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                                                                                                                                                                                                                            (first entry)
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The invention relates to a novel method for determining a subject's susceptibility to the early onset or progression of an ageing-related condition (EOA). The novel method comprises assessing the subject's genotype with respect to at least one allele of an interleukin (IL)-1 pattern 2 and/or pattern 3 (the presence or absence of at least 1 allele provides information about the subject's susceptibility to an early onset or progression of an ageing-related condition). The method is useful for determining or predicting a subject's susceptibility to the stropprosis, osteoperathitis, wrinkled skin, or age-related cancer) and carly onset or progression of an ageing-related condition (e.g. of thermining an ageing-related phenotype. The method may be a customised therapy based on the individual's genetic profile, to tailor a recommended lifestyle, including changes in exercise and diet, and to recommend mutraceuticals that are predicted to benefit a subject having a particular IL-1 genotype and BOA predisposition. This polymucleotide sequence relating to the Disclosure; Fig 5; 98pp; English

Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;

ö 8464 8524 8584 8644 8764 8884 9124 8704 8944 9004 9064 ACAGAAGGATATTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGGAGTCAG 9184 9244 8824 840 9304 420 180 240 300 360 480 540 009 999 780 900 960 09 8465 CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGGTCAG 8345 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 8405 AACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 8585 CTACTCACTTAAAGCCCGCCTGACAGAAACCACGGCCACACTTTGGTTCTAAGAAACCCTC 8705 GTTTGTTTTGATTCATTGGTCTAATTTATTCAAAGGGGGCCAAGAAGTAGCAGTGTCTGTA 8825 AAATCAAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATTATTAAATGGGAATA 8885 TITATAAATGAGCAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA AAAAAAAAGGGTCTCTCCTGATCATTGACTGTCTGGATTGACACTGACAGTAAGCAAAC 9065 GAAATATCCTTGGCCACCGAAGACTATCCTCCTCACCCATCCCCTTTATTTCGTTGTTCA GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAACATCTTTGAGCAAC 1 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGAACTCCAATCCCTAGGGCTGGCAGAAAGGG 61 AACAGAAAGGITITIGAGIACGGCIAIAGCCIGGACTITCCIGITGICIACACCAAIGCC CTCTCTCTCTTTCAGGGCCAATCCCCAGCCCTTTTGTTGAGCCAGGCCTCTCTCACCTCTCTC 8525 CTCTCTCCTTTCAGGGCCAATCCCCAGCCCTTTTGTTGAGCCAGGCCTCTCTCACCTCTC CTACTCACTTAAAGCCCGCCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCTC AAATCAAGTCCTTTAATTAACACTGAAAATATATATAAGCTCAGATTATTAAATGGGAATA AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTGCTGAGTGCTGCAAGTACCTA GAAATATCCTTGGCCACCGAAGACTATCCTCCTCACCCATCCCCTTTATTTCGTTGTTCA **ACAGAAGGATATTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG** GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAACATCTGTTGAGCAAG CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCACAAGTCCCTCCTCAGAT cechanemacaechecaegnacaeancaeacaeacaercaeacaecaechecaechecae Gaps GTTTGTTTTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA ITTATAAATGAGCAAATATGATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA **AAAAAAAAGGGTCTCTCTGATCATTGACTGTCTGGATTGACACTGACAGTAAGCAAAC** ; 9721; Length Indels AGGAGAGGCAGTTATAAGCAGAACAAGGTAACATGAC 1001 AGGAGAGGCAGCTATTATAAGCAGAACAAGGTAACATGAC 9345 99.7%; Score 997.8; DB 7; 99.8%; Pred. No. 7.8e-235; ive 0; Mismatches 2; Query Match
Best Local Similarity 99.8
Matches 999; Conservative 181 241 8765 541 121 301 361 421 481 8945 661 9005 721 9125 841 9185 9245 9305 601 781 901 961 d g g a g Ωþ g à ò ò ⋧ q ò ઠ à g à à g 유 g 셤 ò $\dot{\delta}$ ∂ ò d ઠ 유 ò 임 ò d

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid, useful for preparing a composition for treating an inflammatory disease or condition associated with increased interleukin production in a human subject, e.g. rheumatoid arthritis or ulcerative
                                                                                                                                                                                                                                                                                                      Interleukin-1 beta; IL-1B; human; single nucleotide polymorphism; SNP; antiinflammatory; nootropic; antirheumatic; antiarthritic; cardiant; antiulcer; ophthalmological; antidiabetic; lipolytic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
replace(3870,t)
/*tag= a
/standard name= "Single nucleotide polymorphism"
/note= "-3737 polymorphic allele 1"
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                                                         ACC83528 standard; DNA; 15402 BP
                                                                                                                                                                                                                                             Human interleukin-1 beta gene
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05-JUN-2002; 2002US-0386020P.
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                                                                                                                                                                                   (first entry)
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Pred. No. 9e-235;
0; Mismatches 2;
99.88;
Best Local Similarity 99.8
Matches 999; Conservative
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RESULT 14

Length 15402;

DB 7;

Score 997.8;

99.78;

Query Match

ВР.

1 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAGGG

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standard; DNA; 29433
          28-JUL-2000 (first entry)
                                                                    WPI; 2000-205971/18.
                                           WO200009525-A2
                                                            (UYEC-) UNIV
                                       Homo sapiens
                                                   03-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a new composition comprising an antisense oligomuclectide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary distress such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the release of deoxyadenosine which activates adenosine receptors causing chosen and inflammation, AAA13512 to AAA3512 to epresent the content of the cont
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                                                                          Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorochioate; impaired respiration; inflammation; allergy; allergy; disease; bronchoconstriction; inhibitor; antinflammatior; antiallergic, antiashmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29433 BP; 8714 A; 6519 C; 5920 G; 8278 T; 0 U; 2 Other;
Human adenosine receptor related polynucleotide SEQ ID NO:2517.
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Gaps

99.7%; Score 997.8; DB 3; Length 29433; llarity 99.8%; Pred. No. 1.1e-234; Conservative 0; Mismatches 2; Indels 0;

Best Local Similarity Matches 999; Conserv

Query Match

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                                                    61 AACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC
                                                                                                                                                           CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG
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Gaps

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Indels

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Similarity

Local

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AAF20950;
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(first entry)

Human interleukin-1 polynucleotide fragment #2517

human, airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; pulmonary hypotromic; pain; cystic fibrosis; allergic rhinitis; pulmonary hypotremsion; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; Low adenosine antisense oligonucleotide; phosphorothioate; allergy; cancer; ss.

Homo sapiens

WO200062736-A2

26-OCT-2000

24-MAR-2000; 2000WO-US008020

99US-0127958P 06-APR-1999;

UNIV EAST CAROLINA. (UYEC-) 1 (NYCE/) 1

Nyce JW;

WPI; 2000-679539/66

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Disclosure; Page 221-227; 1592pp; English

The present invention describes low adenosine (A) content antisense oligonuclectides and compositions (I) comprising them. In the antisense cligonuclectides the A is replaced by a 'Universal' or alternative base. (II) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with ungivespiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, chemokines, endogenously produced specific and non-specific enzymes, chemokines, endogenously produced specific and non-specific enzymes, chemokine receptors, adenosine receptors, bridding proteins, adhesion molecules and their receptors, cytokines and chemokine receptors, adenosine receptors, bridding proteins and enzipheral nervous and non-nervous system certainstiters, defensing and malignancy associated proteins. The antisense oligonucleotides may be used in this way to trast disorders condition selected from pulmonary vasociated proteins and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasociated with a disease or condition selected from pulmonary vasociated with a disease or condition selected from pulmonary vasociated with a disease or condition selected from pulmonary vasociated with a disease or condition selected from pulmonary vasociated by pulmonary disease (CPD), pain, cystic fibrosis (CP), allergic rhinitis (AR), pulmonary impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CP), allergic rhinitis (AR), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or the present invention present invention

Sequence 29433 BP; 8714 A; 6519 C; 5920 G; 8278 T; 0 U; 2 Other;

Length 29433;

DB 3;

997.8;

Score

99.78;

Query Match

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2, 2004, 11:27:15 completed: July Search

Job time : 467 secs

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CD367424 UI-H-FT11-
CD368888 UI-H-FT11-
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                                                                                                2, 2004, 10:39:01 ; Search time 2592 Seconds (without alignments) 11532.424 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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VERSION		62	GI:23	2928	343	
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	Hew		ntheri	.,	Catarrnini	nidae;

Email: cgapbs-remail.nih.gov
Tissue Procurement: Robeff-Pamela, U of I
conA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 705)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

BU626628 CD367424 CD368885 CD370914

113 144 144

705 777 618 618

59.5 59.5 59.3

595.4 595.4 593.8 593.8

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CD367424
UI-H-FTI-bjr-k-07-0-UI.S1 NCI CGAP FT1 Homo sapiens CDNA clone UI-H-FT1-bjr-k-07-0-UI3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Irisue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Eibrary Arrayed by: Dr. M. Bento Soares, University of Iowa

clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

seq primer: M13 FORMARD

POLYA=Yes:
                                  72 TITATAAATGAGCAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. . (bases 1 to 777) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  541 TITATAAATGAGCAAATATGATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA
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Unpublished (1997)
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AUTHORS
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                                                                                                                                                  /clone="UT-H-FTO-Nam-1-22-0-UI"
/tissue type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="Dr2dn: Lung; Vector: pT713-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
NCI CGAP FTO is a cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CNA synthesis was primed with an oligo-dT primer containing a Not 1 site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I; and cloned directionally into pT713-pac vector. The oligonuleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCGC. The cell line was provided by Gary W. Hunninghake from the University of
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TAG_LIB=UI-H-FT0
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                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Seg primer: M13 FORWARD POLYA=Yes.
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                                                                                    /mol type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FI1-blx-d-03-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B" (Life Technologies)"
                                                                       /organism="Homo sapiens"
                       location/Qualifiers
POLYA=Yes
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FT1 Homo sapiens cDNA clone
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Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repeitive elements were found in this CDNA
sequence: 221-272, >(TPAA)n#Simple_repeat
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/tissue_type="Aveolar Macrophage" |
/dev_stage="Aveolar Macrophage" |
/dev_stage="Aveolar Macrophage" |
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/clone_lib="NCI CGAP_FTI" |
/clone_lib="NCI CGAP_FTI" |
/clone_modified polylinker; Site_1: EOR I; Site_2: Not I;
modified polylinker; Site_1: EOR I; Site_2: Not I;
NCI CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996 First strand CDNA synthesis was primed with an oligo-off primer containing a Not I site. Double stranded cDNA was ligated to an ECCR I adaptor, digested with Not I, and cloned directionally into prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dI)18 tail. The sequence rag for this library is GGCCATGCG. The University of Iowa.
TAG_LISSUE-Humman Lung Aveolar Macrophage
TAG_LIB-UT-H-FTI
TAG_SEQ-GGCCATGCCG"
                                                                                                                                                                                                           CD370914 618 bp mRNA linear EST 29-MAY-2003 UI-H-FTI-bjz-j-02-0-UI.S1 NCI CGAP FTI Homo sapiens cDNA clone UI-H-FTI-bjz-j-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
Seq primer: M13 FORWARD
POLYA-Yes.
72 TITATAAATGAGCAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 13
                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo. [1 (Dases 1 to 618)]
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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Best Local Similarity 99.5%; Pred. No. 7.1e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="teaxon:9606"
/clone="Ul-H-FT1-bjz-j-02-0-Ul"
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CD370914.1 GI:31155004
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7;

Indels 1; Gaps

GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Produrement: Robeff-Pemela, U of I

Tissue Produrement: Robeff-Pemela, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
The Dr. M. Bento Soares, Dr. M. Bento Soares, Dr. M. Bento Soares, Dento-soares@ulowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA431510

G68 bp mRNA linear EST 07-NOV-2002
UI-H-FT0-bhm-i-17-0-UI.s1 NCI CGAP_FT0 Homo sapiens cDNA clone
UI-H-PT0-bhm-i-17-0-UI 3', mRNA sequence.
CA431510.1 GI:24794230
120
                                                                                                                                                                                                                                                                                                                492
                                                                                                                                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 GTTTGTTTT-ATTCATTGGTCTAATTTAAAGGGGGGCCAAGAAGTAGCAGTGTCTGTA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTTCGACTGGTGTGTCTCTTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 AAATCAAGTCCTTTAATTAAGACTGAAAATATATAAAGCTCAGATTATTAAATGGGAATA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 TITATAAATGAGGAAATATCATACTGTTCAATGGTTCTGAAAATAAACTTCACTGAAGAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 668) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                            121 CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371 CTACTCACTTAAAGCCCGCCTGACAGAAACCAGGCCACATTTGGTTCTAAGAAACCCTC
                                                                                                                                                                                 61 AACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC
                                                                                                                                                                                                                                                                    551 AACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               491 CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GITIGITITGATICALTGGTCTAATTTATTCAAAGGGGGCCAAGAAGTAGCAGTGTGTA
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
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/tissue type="Aucolar Macrophage"
/day stage="Aucolar Macrophage"
/day stage="Aucolar Macrophage"
/day stage="Aucolar Macrophage"
/day stage="Aucolar Macrophage"
/dlone lib="NOT CGAP FTI"
/dlone lib="NOT CGAP FTI"
/note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: Sock I; Site_2: Not I;
NCI CGAP FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is dignally and the first strand was provided by Dr. Gary W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
                                                                                                                                                                                                                                       CA307004 671 bp mRNA linear BST 01-NOV-2002 UI-H-FTI-bhu-c-24-0-UI.s1 NCI CGAP_FTI Homo sapiens cDNA clone CDI-H-FTI-bhu-c-24-0-UI.3', mRNA sequence.
72 TITATAAATGAGCAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryoffan, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
I (basea 1 to 671, May nobi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from Dr. M. Bento Scares, bento-scares@ulowa.edu
The following repetitive elements were found in this cDNA
Sequence: 221-272, S(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA-PROMERTIANS TO SET TO SET TO SET TO SET T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Length 671;
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TAG TISSUB-Human Lung Aveolar Macrophage
TAG_LB=UT-H-FT1
TAG_SEQ=GGCCATGCCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.5%; Pred. No. 6.8e-108;
Matches 606; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="UI-H-FT1-bhu-c-24-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .671
                                                                                                                                                                                                                                                                                                                                                         CA307004.1 GI:24470058
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Homo sapiens
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                                                         601 AAAAAAAA 609
                                                                                                              12 AAAAAAAA 4
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CA307004/c
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
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                                                                                                           셤
                                                                                                                                                                                         /dev stage="Adult"
//lab host="NulloB (Life Technologies)"
//lab host="NulloB (Life Technologies)"
//cloe=11b="NcI CGAP_FTO"
//cloe=10pgan: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP_FTO is a cDNA library constructed from a pool of NCI CGAP_FTO is a cDNA library was constructed from a pool of SI RNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  first-strand cDNA contains a library tag sequence that is located between the Nor I site and the (dI)18 tail. The sequence tag for this library is GGCQATGCCG. The cell line was provided by Gary W. Hunninghake from the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITATAAAIGAGCAAATAIGATACIGITCAAIGGITCIGAAAIAAACITCACIGAAGAAA 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 593.8; DB 14; Length 668; 
Pred. No. 6.8e-108; 0; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG TISSUE-Human Lung Aveolar Macrophage
TAG LIB=UI-H-FT0
TAG SEQ=GGCCATGCCG"
                                                                                                                                        /clone="UI-H-FT0-bhm-i-17-0-UI"
/tissue_type="Alveolar Macrophage"
                                                            'organism="Homo sapiens"
                                                                                         Ltype="mRNA"
xref="taxon:9606"
     Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 59.3%; al Similarity 99.5%; 606; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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/dione="UTH-FPO-Num-g-02-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Mault"|
/dev_stage="Mault"|
/dev_stage="Mault"|
/dev_stage="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/loce="Dragn: Lung; Vector: pT773-pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
NCI CGAP FT0 is a cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with an oligo-dT primer containing a Not I site. Double first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCC. The cell line was provided by Gary W. Hunninghake from the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC 120
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MaG IISSUE-Human Lung Aveolar Macrophage
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               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 99.5
Matches 606; Conservative
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robeff-Peamel U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequenoing By: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soaresdulowa.edu
The following repetitive elements were found in this CDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
POLYA=Yes.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG
                                                                                            AACAGAAAGGITITIGAGIACGGCIAIAGCCIGGACITICCIGIIGICIACACCAAIGCC
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LOCUS DEFINITION

ACCESSION

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RESULT 7

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

FEATURES

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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Robeff-Pamela, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
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                          CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 180
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 706)
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                                                                                                                                                                                                                                                                                                      CTACTCACTTAAAGCCCGCCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCTC
                                                                                                                                                                                                    CTCTCTCTTTCAGGGCCAATCCCCAGCCCTTTTGTTGAGCCAGGCCTCTCTCACCTCTC
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The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
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BU626909.1 GI:23293124
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/ lab_host="DAtvectar macrophage" |
/ lab_host="DH10B (Life Technologies)" |
/ clool_lib="MOT_CGAP_FTO" |
/ clool_lib="MOT_CGAP_FTO" |
/ note="Organ: Liung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; Not I; Not I |
/ NCI CGAP_FTO is a cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, e:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I; and cloned directionally into PT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The cell line was provided by Gary W. Hunninghake from the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robeff-Pamela, U of I
Tissue Procurement: Robeff-Pamela, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLONA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this CDNA
sequence: 221-272, "(TAAA) n#Simple_repeat
DOLYA=Yes.
                                                                                                                                                                            BU626613 704 bp mRNA linear EST 23-SEP-2002 UI-H-FTO-bhm-j-10-0-UI.S1 NCI CGAP_FTO Homo sapiens CDNA clone UI-H-FTO-bhm-j-10-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 704)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP inttp://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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Pred. No. 6.6e-108;
0; Mismatches 2; Indels
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TAG_LIB=UJ-H-FT0
TAG_SEQ=GGCCATGCCG"
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/mol_type="mRNA"
/b_xref="taxon:960"
/clone="UI-H-FT0-bhm-]-10-0-UI"
/tissue_type="Alveolar Macrophage"
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llarity 99.5%;
Conservative 0
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TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"
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Unpublished (1997)
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Best Local Similarity 99.5
Matches 606, Conservative
601 AAAAAAAA 609
                                                                 12 AAAAAAAA 4
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TAG_LIB=UI-H-FT0
TAG_SEQ=GGCCATGCCG"
                                                                                                /clone="UI-H-FTO-bhn-h-03-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_srage="Mdult"
/lab_host="DH10B (Life Technologies)"
                              type="mRNA"
xref="taxon:9606"
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/tissue type="Aveolar Macrophage"
/dev stage="Adult"
/dev stage="Adult"
/done lib="Mort Cape FTT"
/done lib="Mort Cape FTT"
/done lib="Mort Cape FTT"
/done lib="Mort Cape FTT"
/done lib="Mort Cape FTT"
/done lib="Mort Cape FTT"
/done lib="Mort Cape FTT"
/done lib="Mort Cape FTT"
/modified polylinker; Site l: EooR I; Site 2: Not I;
Mort Cape FTT is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6: 791-86, 1996. First strand cDNA synthesis was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6: 791-86, 1996. First strand cDNA synthesis was primed with no ligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EooR I adaptor, digested with Not I, and cloned directionally into pyT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCAPGCG. The University of Iowa.

Hunninghake of the University of Iowa.

TAG TISSUE-Hunna Lung Aveolar Macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Producement: Dr. Gary W. Hunninghake, U of I
Tissue Producement: Dr. Gary W. Hunninghake, U of I
Tissue Producement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soaresGulowa.edu
The following repetitive elements were found in this CDNA
sequence: 221-272, >(TAAA) n#Simple_repeat
BOLYA=Yes.
CA305984 1767 bp mRNA linear EST 01-NOV-2002 UI-H-FTI-bhs-f-05-0-UI.sl NCI CGAP FT1 Homo sapiens cDNA clone UI-H-FTI-bhs-f-05-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I Chases I to 76% I to
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1. 767
/ organism="Homo sapiens"
/ dol_type="mRNA"
/ db & xref="taxon:9606"
/clone="UI-H-FT1-bhs-f-05-0-UI"
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/mol_type="mRNA"
/do xref="taxon:9606"
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/tissue_type="Fibrosarcoma"
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/clone lib="NCI CGAF_FSI"
/clone lib="NCI CGAF_FSI"
/clone lib="NCI CGAF_FSI"
/clone Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the CGT) B tail. The sequence tag for this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CAACTGCCTTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.5%; Pred. No. 6.4e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library is GTTCTACGAG.
TAG TISSUE=fibrosarcoma
TAG_LIB=UI-H-DP0
TAG_SEQ=GTTCTACGAG"
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mary Hendrix

Tissue Procurement: Dr. Mary Hendrix

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soaresœuiowa.edu

The following repetitive elements were found in this CDNA
sequence: 221-272, >(TAAA) n#Simple_repeat

POLYA=Yes.
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1 (bases 1 to 767)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
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FEATURES

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Produrement: Robeff-Pamela, U of I
Tissue Produrement: Robeff-Pamela, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@wiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, TCAAA) n#Simple_repeat
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NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                          371 CTACTCACTTAAAGCCGCCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCTC
                                                                                                                                                                                                          251 GITTGTTTT-ATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGGGTCTGTA
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/wol_type="mRNA"
/wol_type="mRNA"
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/clone_lib="NCI CGAP_FS1"
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/clone_lib="NCI CGAP_FS1"
/clone_lib="NCI CGAP_FS1"
/clone_lib="NCI CGAP_FS1"
/clone_lib="nci Fibrosarcoma Cell line HT-1088 (ATCC number CCL-121). The library was constructed according to Bonaldo, lennon and Soares, Genome Research, 6:791-806, 1996. First strand containing a Not I site Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonacleotide used to prime the synthesis Pac vector. The oligonalcetide used to prime the synthesis of first-strand contains a library tag sequence that is located between the Not I site and the (dT) l8 tail. The sequence tag for this
                                                     %Q000281
770 bp mRNA linear EST 17-JUN-2002
71-H-DPO-avt-c-13-0-UI.sl NCI_CGAP_Fs1 Homo sapiens cDNA clone
.WAGE:5883972 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Itsue Procurement: Dr. Mary Hendrix

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Expending by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.lnl.gov

The following repetitive elements were found in this CDNA Seq primer: M13 FORWARD

POLYA-Yes.
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                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (Dases 1 to 770)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library is GTTCTACGAG.
TAG_TISSUE=fibrosarcoma
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TAG_LIB=UI-H-DP0
TAG_SEQ=GTTCTACGAG"
                                                                                                                                     BQ000281.1 GI:19725181
EST.
                                                                                                                                                                                                        sapiens (human)
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Best Local Similarity
Matches 606; Conserv
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR 1; Site_2: Not 1; Not 1: CGAP FT0 is a cDNA library constructed from a pool of 81 ENA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dfr primer containing a Not 1 site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not 1, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (df)18 tail. The sequence tag for this library is GGCOATGCGG. The cell line was provided by Gary W. Hunninghake from the University of
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                                                                                                                                                                                                                                                                                             TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI.H-FT0
TAG_SEQ=GGCCATGCCG"
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EST 01-NOV-2002

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798 bp

CA307234

RESULT 14 CA307234/c LOCUS

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Tunour Gene Index
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this CDNA
sequence: 221-272, >(TRAA) n#Simple_repeat
Seq primer: M13 FORWARD
POUXA=Yes:
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NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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UI-H-FT1-bhu-p-02-0-UI.81 NCI CGAP FT1 Homo sapiens cDNA clone
UI-H-FT1-bhu-p-02-0-UI 3', mENA sequence.
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59.3%; Score 593.8; DB 14; Length 798;
Best Local Similarity 99.5%; Pred. No. 6.3e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                 CA307234.1 GI:24470288
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Search completed: July 2, 2004, 13:27:46 Job time : 2598 secs
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Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.B. Consortium/LiML at: http://mage.llnl.gov

The following repetitive elements were found in this cDNA

Sequence: 221-222, S(TAAA)n#Simple_repeat

POLYA-Yes.
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INAGE:5892524 3', mRNA sequence.
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                     CTCTCTCTTTCAGGCCAATCCCCAGCCCTTTTGTTGAGCCCAGGCCTCTCTCACCTCTC 372
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                                                                                       CTACTCACTTAAAGCCCGCCTGACAGAACCACGCCACATTTGGTTCTAAGAAACCCTC 312
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/dev_stage="Adult"
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/lab_host="NHIOB (Life Technologies)"
/clone_lib="NCI_CGAP_DHI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Cases 1 to 703)

NCI-CAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                             CTACTCACTTAAAGCCCGCCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCTC
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modified polylinker; Site_1: ECOR I; Site_2: Not I; NOT ICAPP DHI is a normalized CDNA library containing the following tissue(s): vS-8 Cell line from Metastatic chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT):18 tail. The sequence tag for this library is AGATCATGC.

TAG_IBBEUI-H-DHI

TAG_ESC-AGATCATTGC.
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March 17, 2003, 20:32:30; Search time 1145 Seconds (without alignments) 5998.482 Million cell updates/sec
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236
1 ttttgattcattggtctaat......ataaacttcactgaagaaaa 236
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

iption	G10509 human STS C AXC27920 Sequence 101156 Sequence 1 K02170 Human monoc E00846 cDNA sequen 107942 Sequence AXC67266 Sequence AXC6726 Sequence AXC6726 Sequence AXC6726 Sequence AXC6726 Sequence AXC6726 Sequence AXC6726 Sequence AXC6726 Sequence AXC6726 Sequence AXC6726 Sequence AXC6726 Sequence AXC6726 Sequence AXC6730 Human inter BC0734 DNA encodin M15330 Human inter BC0734 DNA encodin AY137079 Homo sapi AC0729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence 100729 Sequence AC11912 AC11912 MXC295 Reabbit inter D21835 Rabbit mRNA AC106390 Rattus no AC090139 Homo sapi AC106390 Rattus no	A linear STS 15-AUG-1995 3 clone UTR_00699_X04500, agged site. dut+ung+ (DH10B) Marker individual of French a; Vertebrata; Euteleostomi;
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e Query re Match Lengi	94 4 8 8 2 9 9 4 8 8 2 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	G10509 human STS CHLC.UTR sequence tagged sij G10509.1 GI:94238(G10509.1 GI:94238(STS, STS sequence; Homo sapiens vecto) selected genomic DB nationality. Homo sapiens Eukaryota; Metazoa Mammalia; Eutheria, 1 (bases I to 614)
Result No. Sco	0 00 0 0 000	RESULT 1 G10509 LOCCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE

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Matches 194; Conservative
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Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.H.
Cooperative Human Linkage Center
Unpublished (1995)
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0
                                  Synonyms: UTR_00699_X04500, CHLC.UTR_00699_X04500.T36097
Contact: Dr. Jeffrey C. Murray
Uofi
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prepared Prepared with primer pairs derived from X04500.
                                                                                                                                                                                                                    30 seconds at 94 degrees C
75 seconds at 55 degrees C
15 seconds at 72 degrees C
27
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                                                                                                                                                                                                                                                                         6 minutes at 72 degress
                                                                            The University of Iowa
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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each 1.5 pmole
each 200 uM
0.3 units
10 ul
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ilarity 100.0%; Pred. No. 1.9e-86;
Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
180. 408
                                                                                                                                                              Primer A: AGTCAGCTCTCTTCAGG
Primer B: CTTGCCCCCTTTGAATAAAT
STS size: 229
PCR Profile:
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Total Vol:
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KCl: 50mM
Tris: 10mM
pH: 8.3
                                                                                                                                         Email: jeff-murray@uiowa.edu
                                                                                                                                                                                                                                                              PCR cycles:
extension:
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Primer:
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PAT 16-SEP-2000

linear

DNA

Sequence 5 from Patent WO0039314.
AX027920.1 GI:10188746

DEFINITION ACCESSION VERSION KEYWORDS

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Unknowu.
Unknowu.

Unclassified.

1 (bases 1 to 1469)

Auron, P.E., Webb, A.C., Gehrke, L., Dinarello, C.A., Rosenwasser, L.J.,
Rich, A. and Wolff, S.M.
Rich, A. and Wolff, S.M.
Truncated protein of interleukin-1
Patent: US 4762914-A 1 09-AUG-1988;

119 Wilson Dr.; Framingham, MA
On Jul 30, 1993 this sequence version replaced gi:285486.

Location/Qualifiers

1 . 1469
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases I to 656)

Kastelic, T. and Cheneval, D.

Assay for identifying compounds which affect stability of mrna Patent: Wo 0039114-A 5 06-UUL-2000;

KASTELIC TANIA (CA); CHENEVAL DOMINIQUE (CA); NOVATION PHARMACEUTICALS INC (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1328 GCCTAGTTTTTAATAGCTATGGAATCAATTTGAATTTGGACTGGTGTGCTCTCTTTTAATC 1387
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iive 0; Mismatches 0;
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PRI 06-JAN-1995

linear

DEFINITION

RESULT 4

ACCESSION VERSION KEYWORDS SOURCE

1448

g ò ORGANISM

REFERENCE AUTHORS

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Eukaryotz, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Makaryotz, Metazoa; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1496)
Webb,A.C., Dinarello,C.A., Rosenwasser,L.J., Mucci,S.F., Rich,A., Wolff,S.M. and Auron,P.E.
Nucleotide sequence of human monocyte interleukin 1 precursor cDNA Adv. Gene Technol. 22, 339-340 (1985)
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Matches 194; Conservative 0; Mismatches 0; Indels
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/gene="ILIA"
/note="interleukin 1 mRNA; G00-120-695"
                                            complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="precursor protein"
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/db_xref="taxon:9606"
/map="2q12-q21"
                 1496 bp
Human monocyte interleukin mRNA,
M54933 M38756
M54933.1 GI:186287
                                                                                                                                                                                                                                                                                                                                                                                                                             type="monocyte"
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cDNA sequence for human
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/gene="IL1A"
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                                                                                                          interleukin 1.
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DGGIQLRISDHHYSKGFRQAASVVVAMDKLRKMLVPCPQTFQENDLSTFFFIFEEP
IFPDFWDNEAYVHDAPVRSLMCTLRDSQQKGIVMSGPYELKALHLQGQDMEQQVVFSM
SFVQGESSNOFNXIPVALGLKEKNLYLSCVLKDDKPTLQLGSVDFKNYPKKKMEKRFVFN
KIEINNKLEFESAQFPRYSTSQAENMPVFLGGTKGGQDITDFTMQFVSS"
1 361 c 328 g 391 t
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cds.
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1 (bases 1 to 149.

Auron, P.E., Webb, A.C., Rosenwasser, L.J., Mucci, S.F., Rich, A., Wolff, S.M. and Dinarello, C.A.

Wolff, S.M. and Dinarello, C.A.

Nucleotide sequence of human monocyte interleukin 1 precursor cDNA Proc. Natl. Acad. Sci. U.S.A. 81 (24), 7907-7911 (1984)
                          1388 AAGTCCTTTAATTAAGACTGAAAATATAAAGCTCAGATTTTAAATGGGAATATTATT 1447
                                                                                                                                                                                                                                                                                                                                           monocyte, cDNA to mRNA, clones pA-26
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    121 AAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATTATTAAATGGGAATATTTAT
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llarity 100.0%; Pred. No. 1.6e-86;
Conservative 0; Mismatches 0; Indels
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/note="interleukin 1 precursor polypeptide"
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/db_xref="taxon:9606"
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/protein_id="AAA36106.1"
/db_xref="G1:307043"
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104 bp upstream of AluI site.
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interleukin; interleukin 1.
Human endotoxin-stimulated
pcD-415 and pcD-1218.
Homo sapiens
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PAT 29-SEP-1997

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           Fuirtesupu, I.A., Chiyaarusu, E.D., Andoriyuu, S.U., Arekisandaa, R., Shierudon, E.U., Rii, G. and Ranii, J.R.
Shierudon, E.U., Rii, G. and Ranii, J.R.
HUMAN IL-ICDNA HAVING BIOLOGICALLY ACTIVE HUMAN IL-1 PROTEINCODE
PACENT: JP 1986119191-A 1 06-JUN-1986;
MASSAGHUSETTS INST OF TECHNOL AMIT>, NEW INGURANDO MEDICAL CENTER
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PC C12N15/00, A61K39/395, C07K13/00, C12N1/00, C12N5/00, C12P21/02,
(C12N1/00,
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                                                                                                          OS Human {Homo sapiens}
PN JP 1986119191-A/1
PD 06-UMY-1986
PF 18-MAY-1985 JP 1985104978
PR 18-MAY-1984 US 84 611669, 11-FEB-1985 US 85
FURRISUPU II AURON, CHIYAARUSU EE DEINARERO, PI A
                                                                                                                                                                                                                                                                                                                                       *source: tissue type=Blood;
*source: cell_type=Monocyte;
Key
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strandedness: Double;
topology: Linear;
hypothetical: No;
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/db_xref="taxon:32644"
361_c 328_g 391
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PAT 02-DEC-1994

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DNA

Sequence 1 from Patent EP 0161901. 107942 107942.1 GI:589345

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1 (bases 1 to 1507)
Muron,P.B., Webb,A.C., Gehrke,L., Dinarello,C.A., Rosenwasser,L.J., Rich,A. and Wolff,S.M.
Human il-1 cDNA sequences encoding biologically-active human il-1
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I (basea I to 972)

Kormman, K. S., Duff, G. W., Crossman, D. C., Francis, S. E. and Stephenson, K.

Diagnostics and therapeutics for restenosis

Patent: WO 0077753-A is 30-NOV-2000;
Interleukin Genetics, inc. (US)
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/organism="Homo sapiens"

/db.xref="taxon:9606"

/note="laxon:9606"

/note="la.1B gene~'n' bases throughout the

A, T, C, G, other or Unknown"

A, T, C, G, other or 2 others
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100.0%; Pred. No. 1.6e-86;
:ive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.2e-86;
Matches 194; Conservative 0; Mismatches 0;
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Location/Qualifiers
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Sequence 16 from Patent W00071753.
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. 361 c 328 g
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Unclassified.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Clark, B.D., Collins, K.L., Gandy, M.S., Webb, A.C. and Auron, P.E.
Genomic sequence for human prointerleukin 1 beta: possible
volution from a reverse transcribed prointerleukin 1 alpha gene
Nucleic Acids Res. 14 (20), 7897-7914 (1986)
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/note="pot. viral enhancer core sequence"
2006. .2465
                                                                                                                                                                  Query Match 82.2%; Score 194; DB 6; Length 97 Best Local Similarity 100.0%; Pred. No. 1.2e-86; Matches 194; Conservative 0; Mismatches 0; Indels
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Doce="direct repeat 2"
2291. .2297
/note="pot. viral enhancer core sequence"
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/clone lib="leukocyte DNA library"
669. .960
/note="Alu repeat"
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note="TATA-box like sequence"
                                                            /organism="Homo sapiens"
/db xref="taxon:9606"
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db_xref="taxon:9606"
chromosome="2"
    , INC. (US)
Location/Qualifiers
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2328 c 2127
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Variants of il-1 beta gene and cd46 gene for diagnosing unexplained
recurrent pregnancy loss
Patent: WO 0222877-A 1 21-MAR-2002;
PHE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); DANA-FARBER CANCER
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1 (bases 1 to 9721)

Duff. G. W., Cox, A., Camp, N.J. and di Giovine, F.S.
Diagnostics and therapeutics for diseases associated with an il-1 inflammatory haplotype
Patent: WO 0100880-A. 2 04-JAN-2001,
Interleukin Genetics, Inc. (US)
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
8770 GCCTAGTITITAATAGCTATGGAATCAATTTCAATTTGGACTGGTGTGCTCTCTTTAAATC 8829
                                                                              8830 AAGICCITIAATIAAGACIGAAATATATAAGCICAGAITATITAAATGGGAATATITAT 8889
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                                         AAGTCCTTTAATTAAGACTGAAAATATATATAAGCTCAGATTATTTAAATGGGAATATTTAT 180
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ive 0; Mismatches
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Sequence 2 from Patent W00100880.
AX067266
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/db_xref="taxon:9606"
2328 c 2122 g 2606
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Sequence 1 from Patent W00222877.
AX469435
AX469435.1 GI:21901721
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                                                                            join(2481. .2527,3092. .3143,5125. .5326,5874. .6038,7275. .7405,8127. .8339)
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complement (6910. .6915)
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complement (6916. .6924)
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complement (747. .7253)
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/note="pot. viral enhancer core sequence"
8127. .8953
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/note="inverted repeat A"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGTCTTTAAATC
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Patent: WO 0198537-A315 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.2e-84;
Matches 189; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 189; Conservative
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Best Local Similarity 100.
Matches 189; Conservative
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Patent: US 5861267-A 10 19-JAN-1999;
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Lomakin,I.B., Emel'yanov,A.V., Kozlov,A.P., Konusova,V.G.,
Kotov,A.Y., Kurbatova,T.V., Reshetnikov,V.L., Simbirtsev,A.S.,
Ketlinskii,S.A. and Vinetskii,Y.P.
Cloning of the cDNA coding for human prointerleukin-1 alpha and
prointerleukin-1 beta
Dokl. Akad. Mauk SSSR 309 (4), 1005-1008 (1989)
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353 c 325 g 387 t
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| db_xref="G1:35663"
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Pred. No. 5.2e-84;
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US 5861267.
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Acrganism="Homo sapiens"
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58. 867
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58. .867
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Sequence 10 from patent
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TITLE
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                                                                                                                                                                                                                                                                                                   CTTTAATTAAGACTGAAAATATATAAGCTCAGATTATTTAAATGGGAATATTATAATG 185
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                                                              Gaps
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                   Length 1497;
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              Score 189; DB 6; Length 14
Pred. No. 5.2e-84;
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/product='IL-1 beta'
Location/Qualifiers
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I (bases 1 to 1497)
Higaki,M., Shoji,Y. and Mizushima,Y.
Higaki,M., Shoji,Y. and Mizushima,Y.
OHOSPHOOLIGONUCLEOTIDE AND ITS USE
Patent: 19 1994041185-A 5 15-FEB-1994;
L T YENNYUSHO:KK
PD 1994041185-A/5
PD 15-FEB-1992
PP 16-JUL1992 JP 1992213519
PP 16-JUL1992 JP 1992213519
PP 16-JUL1992 JP 1992213519
PP 16-JUL1992 JP 1992213519
PP 16-JUL1992 JP 1992213519
PP 11GAKI MEGUMI, SHOJI YOKO, MIZUSHIMA
COTH21/04,A6IK31/70,A6IK31/70,C12P19
CC strandedness: Double;
CC topology: Linear;
FH Rey 1. 14997
FT mat_peptide 1. 14997
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365 c 331 g
80.1%; Scc...
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Oy 186 AGCAAATAT 194 ||||||||| Db 1451 AGCAAATAT 1459

Search completed: March 17, 2003, 21:05:13 Job time : 1157 secs

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Interleukin-1 beta; IL-1B; human; polymorphism; inflammation; coronary artery disease; osteoporosis; nephropathy; alopecia areata; Graves disease; systemic lupus erythematosus; lichen sclerosis; ulerative colitis; diabetic retinopathy; periodontal disease; juvenile chronic arthritis; psoriasis; insulin dependent diabetes; asthma; lung fibrosis; chronic inflammatory liver disease; rheumatoid arthritis; chronic inflammatory lung disease; antiinflammatory; osteopathic; dermatological; immunosuppressive; antiinflammatory; osteopathic; dermatological; immunosuppressive; antiinflabetic; antithyroid; hepatotropic; antiulcer; diagnosis; therapy; ds.
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ABN38537
AAAS0182
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AAQ05593
AAX02995
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AAD35192
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ABK50291
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Human interleukin-
Human interleukin-
Human IL-1B gene.
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14. SIDS2/gcddata/geneseq/geneseqn.embl/NA1992.DAT:*

15. SIDS2/gcgdata/geneseq/geneseqn.embl/NA1992.DAT:*

16. SIDS2/gcgdata/geneseq/geneseqn.embl/NA1992.DAT:*

17. SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

18. SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

20. SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

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24. SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                    US-09-247-874C-2_COPY_8710_8945
236
1_ttttgattcattggtctaat......ataaacttcactgaagaaa 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                     GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                            2185239 segs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                         nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAS0175
AAAS1659
AAF20946
AAA34824
AANS0060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC50981
AAX75924
AAF20945
AAC63768
                                                                                                                                                                                                                                                                                                                                                    Gapop_60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Geneseq 101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Result Š 2336 1199444 11994444 11994444

10m450r86

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Human gene signatu
Sequence encoding
Sequence encoding
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Human

Human ILIB gene. Human interleukin Human interleukin Human IL-1ra BAC c

Interleukin 1-beta 3' UTR cDNA.

31-OCT-2000 (first entry)

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Novel methods and nucleic acids for diagnosing and treating disorders associated with high levels of interleukin lbeta, especially inflammatory diseases -
                          (INTE-) INTERLEUKIN GENETICS INC.
                                                                               Claim 34; Fig 2; 74pp; English
    10-FEB-2000; 2000WO-US03443
                                    Di Giovine FS
                                               WPI; 2000-558192/51.
               10-FEB-1999;
                                     3
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The present sequence is that of human interleukin-1 beta (IL-IB) allele 2 (+6912), which is a form of the IL-IB gene that contains guanine at position (see AAA50124). The invention is based on the identification of this novel allele at marker +6912 of the IL-IB gene. The C to G translation occurs within the 3 untranslated region of the IL-IB gene and results in an increased level of IL-IB protein. Individuals homozygous for the IL-IB allele 2 (+6912) crowided for detecting IL-IB allele 1 (+6912). Methods and kits are provided for detecting IL-IB allele 2 (+6912), or an allele in than homozygotes for IL-IB allele 2 (+6912), or an allele in the Inkaged eisequilibrium with an IL-IB allele 2 (+6912), and thereby determining a patient's susceptibility to developing inflammatory disorders, especially coronary artery disease, oreopozosis, nephropathy in diabetes mellitus, alopecia areata, divenile chronic arthritis, psortasis, insulin dependent diabetes, asthma, chronic arthritis, psortasis, insulin dependent diabetes, asthma, chronic inflammatory liver disease, ch

Sequence 9721 BP; 2661 A; 2327 C; 2123 G; 2608 T; 2 other;

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                                                                                                                                        8710 TITIGATICATIGGICTAATITATICAAAGGGGGAAGAAGIAGCAGTGICIGIAAAAGA 8769
                                                                                                                                                                                                                                                                                                                                  8830 AAGTCCTITAATIAAGACTGAAAATATATAAGCTCAGATTATTTAAATGGGAATATTTTA 8889
                                                                                                                                                                                                                                              GCCTAGITITITAAIAGCIAIGGAAICAAIICAAITIGGACIGGIGIGCICICITITAAAIC 8829
                                                                                                                                                                                              GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTCTTTAAATC 120
                                                                                                                                                                                                                                                                                            AAGTCCTTTAATTAAGACTGAAATATATATAGCTCAGATTATTTAAATGGGAATATTTAT 180
                                                                                                  TITIGATICATIGGICIAATITATICAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA 60
                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     8890 AAATGAGCAAATATGATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAAAA 8945
                                                                                                                                                                                                                                                                                                                                                                                       181 AAATGAGCAAATATGATACTGTTCAATGGTTCTGAAATAAAACTTCACTGAAGAAAA 236
100.0%; Score 236; DB 21; Length 9721; 100.0%; Pred. No. 3e-106; ive 0; Mismatches 0; Indels 0;
                              Best Local Similarity 100.
Matches 236; Conservative
          Query Match
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AAAS1659 standard; cDNA; 656 BP

AAA51659

RESULT 2
AAA51659
ID AAA5
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AC AAA5
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This is the 3' UTR of interleukin 1-beta mRNA which contains AU-rich element (ARE) motifs. These ARE motifs are found in genes subject to mRNA instability. Identification of a compound which affects mRNA stability comprises a DNA expression system which in the absence of the test compound is capable of expressing a protein having a detectable signal. The mRNA which codes for the protein, and which is transcribed from the expression system, comprises at least one copy of a mRNA instability sequence. The mRNA is contacted with a test compound and the detectable signal is measured in the presence of the test compound and compared with a control. Compounds identified by the new method can be used for the treatment of a disease or medical condition which involves inappropriate mRNA stabilization and/or accumilation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying compounds which affect mRNA stability for the treatment of disease e.g. arthritis comprises a DNA expression system expressing a protein having a detectable signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 489 eccraentrinanaecrareeaarcaarteaarreaecreereererererrinaare 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATTATTAAATGGGAATATTTAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429 TTTTGATTCATTGGTCTAATTTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAGA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     undesirable protein expression (claimed) e.g. rheumatoid arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTCTTTAAATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
82.2%; Score 194; DB 21; Length 656;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels (
                                                               IL-1-beta, 3' UTR; interleukin 1-beta, AU-rich element; ARE mRNA instability; rheumatoid arthritis; osteoarthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 656 BP; 176 A; 151 C; 129 G; 200 T; 0 other;
                                                                                                                                                                                                                                                                                           406..414

/*tag= c

/*tote= "Minimal instability motif"

644..649

/*tag= d
                                                                                                                                                                                          *tag= a
'rpt_type= TANDEM
'note= "3 copies of AU-rich motif"
                                                                                                                                                                                                                                   404..408
/*tag= b
/note= "AU-rich motif"
                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 1, 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98GB-0028709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVA-) NOVATION PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                       WO200039314-A1
                                                                                                                                                                         repeat_region
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                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                   polyA_signal
                                                                                                                       Homo sapiens
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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and crivating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Low adenosine antisense oligonucleotide; phosphorothioate, allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antihilammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; panh; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptors, CNS and peripheral nervous and non-nervous system peptide transmitters. defensings, growth factors, vascactive peptides and receptors, binding proteins and mailgnancy associated proteins and mailgnancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -
549 AAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATTATTTAAATGGGAATATTTAT 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human interleukin-1 polynucleotide fragment #2513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 232-233; 1592pp, English.
                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                  AAF20946 standard; DNA; 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-2000; 2000WO-US08020
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(NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                       AAATGAGCAAATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF20946;
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condition selected from pulmonary vasoconstriction, inflammation, allegies, asthma, impeded respiration, respiratory dispurses syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplanterion rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21843 represent human polymucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphorothioate, impaired respiration, inflammation, allergy, allergy allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic, antiasthmatic; cytostatic; analgesic; impaired airway, lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1389 AAGTCCTTTAATTAAGACTGAAAATATATATAAGCTCAGATTATTTAAAATGGGAAATATTTAT 1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1269 TITIGALICATIGGICTAATITTATICAAAGGGGCCAAGAAGIAGCAGIGICTGTAAAAGA 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTCTTTAAATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AAGTÇÇTTTAATTAAGAÇTGAAAATATATAAGÇTÇAGATTATTTAAATGGGAATATTAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; adenosine receptor; low adenosine antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TTTTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human adenosine receptor related polynucleotide SEQ ID NO:2513.
                                                                                                                                                                                                                                                                                                                                                                                                      Length 1496;
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                                                                                                                                                                                                                                                                                                                             Sequence 1496 BP; 416 A; 361 C; 328 G; 391 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                              82.2%; Score 194; DB 21; 100.0%; Pred. No. 1.3e-85; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 675; 1343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР.
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Matches 194; Conservative
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                                                                                                                                                                                                                                                       the present invention.
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       The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which transpers nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antininflammatory, antiallergic, antialmention, antialmention, antialmention, antialmention, antialmention, antialmention, antialmention are useful for the treatment of diseases associated with inflammation. The COM can have antininflammatory, antiallergic, antialment of impaired airways, including lung disease associated with inflammation, effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the relaction of adexyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA33313 to AAA33312 represent the nucleotide sequences given in the sequence listing from the present intention, which correspond to SEQ ID NO:11 to 16% but the sequences differ from the previously named sequences. SEQ ID NO:11 to 16% invention, and inflammation, and with their corresponding SEQ ID NO: sequences in the sequence of the present invention do not match up with their corresponding SEQ ID NO: sequences.
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Pred. No. 1.3e-85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1496 BP; 416 A; 361 C; 328 G; 391 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.2%; Score 194; DB ilarity 100.0%; Pred. No. 1.3 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence encoding interleukin-1 (IL-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATGAGCAAATAT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAY-1985;
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                                                                                                                                                                                                                                                                                                     A pure cDNA of 1507 bp (AAN50060) (and its 1-606, 1-677, 1355-1507; 482-477; and 1355-1507 tragments) are claimed. Also claimed is a recombinant DNA cloning vehicle contg. the human IL-1 gene sequence. Specifically the vehicle contains the sequence coding for the new 287 AA sequence (AAP50043) or the following new fragment (1) 9-224; (2) 1-210-X; (3) 144-287; and (4) 144-210-(X); (X= Asn-11e-Thr-Thr-Gly-Val-Leu-Ser-Leu-Asn-Gln-Val-Leu).
                                                                                                                                                                                    Recombinant cloning vehicle contg. human interleukin-7 gene-or its
fragments, producing new biologically active polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATTATTAAATGGGAATATTTAT
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/product= hIL-1
/note= "N- and C-terminally truncated forms of
/note= "N- sequence which retain IL-1 activity
are covered by the invention"
                                             Rosenwasser LJ,
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C-terminal deletion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1507;
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Pred. No. 1.3e-85;
                                             Dinarello CA,
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100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                                                                                                                                                                                             Claim 7; Page 34-35; 39pp; English
                                               Gehrke L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ50981 standard; cDNA; 1507
(NEWE ) NEW ENGLAND MED CEN.
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Best Local Similarity 100.0
Matches 194; Conservative
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                                                                                                                WPI; 1985-291135/47.
P-PSDB; AAP50043.
                                               Webb AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                             PE,
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Auron PE, Webb AC,

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The present invention describes genotyping a nucleic acid sample from a subject to determine at least one allele of an interleukin-1 (IL-1) prolifiammatory haplotype. A method has also bee described for determining a subject's susceptibility to developing chronic obstructive airway disease (COAD) or for predicting the rapidity or ultimate progression of a COAD in the subject; by: (a) obtaining a mucleic acid sample from the subject, and (b) detecting at least one allele of an IL-1 proinflammatory haplotype in the sample, where detection of at least one of these alleles indicates that the patient has an increased susceptibility to developing COAD. The method is useful for determining the susceptibility of subjects to developing chronic obstructive airway disease or for predicting the rapidity or ultimate progression of chronic obstructive airway disease (COAD). COAD can be asthma, emphysema, chronic bronchification of chronic obstructive airway disease (COAD), carriage, thereby increasing the probability of a positive outcome. The stage, thereby increasing the pubmbility of a positive outcome. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; andlgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration, surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8830 AAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATTATTAAATGGGGAATATTTAT
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                                                                                                                                                                                                          Genotyping nucleic acid samples for interleukin-1 (IL-1) proinflammatory haplotype alleles, useful for predicting susceptibility to developing chronic obstructive airway disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human interleukin-1 polynucleotide fragment #2512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.2%; Score 194; DB 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0;
                                                                                                                     Lim S;
                                                                                                                  Barnes PJ, Duff GW, Glovine M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF20945 standard; DNA; 9721 BP.
                                                                     (MEDI-) MEDICAL SCI SYSTEMS INC
                                                                                                                                                                                                                                                                                                           Example 1; Fig 2; 37pp; English
                      97GB-0023553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AAATGAGCAAATAT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATGAGCAAATAT
                                                                                                                                                               WPI; 1999-327420/27
12-JAN-1998;
07-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF20945;
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  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1329 GCCTAGTTTTTAATAGCTATGGAATCAATTTGGACTGGTGTGCTCTTTTAAATC 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA comprising part of the nucleotide sequence AAQ50981 which encodes a polypeptide having IL-1 activity and a mol.wt. of 20000 is claimed. Specifically, the region between nucleotides 111-717 has been found to retain hIL-1 activity (see AAQ45464).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GCCTAGTTTTTAATAGCTATGGAATCAATTTGGACTGGTGTGCTCTTTTAAATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; interleukin 1; IL-1B; IL-1R); diagnosis; detection;
chronic obstructive airway disease; chronic bronchitis; emphysema;
asthma; chronic bronchiolitis; proinflammatory haplotype; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AAGTCCTTTAATTAAGACTGAAAATATATAAAGCTCAGATTATTTAAATGGGAATATTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                   New DNA encoding protein with IL-1 activity - useful in monitoring disease states e.g. cancer and studying inflammation
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                                                                                                                                                                                                                                                            Rosenwasser LJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1507 BP; 427 A; 361 C; 328 G; 391 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 194; DB 14;
Pred. No. 1.3e-85;
                                                                                                                                                                                                                                                            Rich A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.2%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                               HOSPITALS
                                                                                                                                    (MASI ) MASSACHUSETTS INST TECHNOLOGY.
(NEWEL) NEW BNGLAND MED. CENT HOSPITAL
(TUTFT ) TUFTS COLLEGE.
(WELL-) WELLESLEY COLLEGE.
                                                                                                                                                                                                                                                            Gehrke L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 11-16; 24pp; English.
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                      85EP-0303234.
                                                                   84US-0611669
                                                                                            85US-0700374
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                                                                                                                                                                                                                                                         Dinarello CA,
Wolff SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. in arthritis etc
                                                                                                                                                                                                                                                                                                                          WPI; 1993-360975/46.
P-PSDB; AAR42213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                      07-MAY-1985;
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                                                                   18-MAY-1984;
                                                                                            11-FEB-1985;
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Query Match Best Local S

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Gaps 9 8829

8889 180

20-MAY-1999

AAX75924;

AAX75924 ID AAX RESULT 7

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respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; Homo sapiens. cancer; ss

WO200062736-A2

24-MAR-2000; 2000WO-US08020.

26-0CT-2000

99US-0127958. 06-APR-1999;

(UYEC-) UNIV EAST CAROLINA (NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions

Disclosure; Page 230-232; 1592pp; English.

oligonucleotides and compositions (1) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. It can have respiratory, bronchodilator, antiniflammatory, analgesic. immunosuppressive, antiathmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (1) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific and confession molecules and chemokine receptors, adhesion molecules and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensints, growth factors, vascative peptides and receptors, binding proteins and maingnancy associated proteins. The antisense oligonuclectides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allegies, asthma, impeded respiration, respiratory discress syndrome (RDS), pain, cystic fibrosis (CP), allergic thinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF1843 to AAF21843 represent human polymuclectide fragments and antisense oligonuclectides used in the exemplification of present invention describes low adenosine (A) content antisense the present invention.

Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;

Gaps . 0 82.2%; Score 194; DB 21; Length 9721; llarity 100.0%; Pred. No. 1.3e-85; Conservative 0; Mismatches 0; Indels 0 Similarity Matches 194; Query Match Local

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8710 TITIGATICATIGGICIAATITATICAAAGGGGGCAAGAAGTAGCAGIGICIGIAAAAGA 8769 9 1 TITIGATICALIGGICIAATITATICAAAGGGGGCCAAGAAGTAGCAGTGTCTGTAAAAGA ð Q

8770 GCCTAGTITITAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTCTTTAAATC 8829 GCCTAGITITITAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTCTTTAAATC 120 61 ઠ q

121 AAGTCCTTTAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTTAT 180

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8770 GCCTAGTTTTTAATAGCTATGGAATCAATTTGGACTGGTGTGCTCTCTTTTAAATC 8829

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. 0 The present sequence is provided in a specification relating to a method for determining whether a subject has or is predisposed to develop an interstital lung disease. The method involves detecting an interleukin-1 receptor antagonist (IL-IRN) (+2018) allele 2, a tumour necrosis alpha (TNF-A)(-308) allele 2, or an allele in linkage disequilibrium with either of these two alleles. The method may be used to determine whether a subject has or is predisposed to develop an interstitial pneumonia or applementy fibrosis and other disorders such as rheumatoid arthritis, systemic lupus erythmatosis, Sjognen's syndrome, systemic sclerosis, dermatcomyocitis. The method is also used for identifying molecules which can be used as therapeutics for treating interstitial lung disease. comprising Human, IL-1B; interleukin-1B; cytostatic; antiinflammatory; immunosuppressive; dermatological; antimicrobial; antiarthritic; IL-1 receptor antagonist; tumour necrosis factor alpha antagonist interstitial lung disease; interstitial pneumonia; pulmonary fibrosis; rheumatoid arthritis; systemic lupus erythmatosis; Sjogren's syndrome; systemic sclerosis; dermatomyocitis; chromosome 2; ds. 8830 AAGTCCTTTAATTAAGACTGAAAATATATAAAGCTCAGATTATTTAAATGGGAATTAT 8889 8710 TTTTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA 8769 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTCTTTAAATC 120 Gaps 1 TITIGATICATIGGICTAATITATICAAAGGGGCCAAGAAGTAGCAGIGTCTGTAAAAGA 60 Method for predicting the risk of interstitial lung disease, compidetecting an interleukin-1 receptor antagonist allele and tumor necrosis alpha allele or an allele in linkage disequilibrium with ; Length 9721; Indels Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other; Query Match 82.2%; Score 194; DB 21; Best Local Similarity 100.0%; Pred. No. 1.3e-85; Matches 194; Conservative 0; Mismatches 0; Whyte M; (INTE-) INTERLEUKIN GENETICS INC. BP Claim 6; Fig 2; 102pp; English. AAC63768 standard; DNA; 9721 31-MAR-2000; 2000WO-US08492. 99US-0286108 08-FEB-2001 (first entry) Duff GW, Di Giovine FS, 8890 AAATGAGCAAATAT 8903 either of these alleles 181 AAATGAGCAAATAT 194 WPI; 2000-656234/63. Human IL-1B gene. WO200060117-A2 Homo sapiens. 02-APR-1999; 12-OCT-2000. AAC63768; 61 RESULT 9 AAC63768 셤 ò ò 셤 δ 0

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181 AAATGAGCAAATAT 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of human interleukin-1 beta (IL-1B) allel 1 (+6912), which is a form of the IL-1B gene that contains cytosine at position +6912; IL-1B allele 2 (+6912) has guanine at this position (see AAASO175). The invention is based on the identification of this novel allele at marker +6912 of the IL-1B gene in the IL-1B gene and results in an increased level of IL-1B protein. Individuals homozygous for the IL-1B allele 2 (+6912) and proximately 4 times more immunoreactive IL-1B protein than homozygotes for IL-1B allele 1 (+6912). Methods and kits are provided for detecting IL-1B allele 2 (+6912), or an allele in thereby determining a patient's susceptibility to developing inflammatory disorders, especially coronary artery disease,
                                                              8830 AAGTCCTTTAATTAAGACTGAAAATATATAAAGCTCAGATTATTTAAATGGGAATATTAT 8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel methods and nucleic acids for diagnosing and treating disorders associated with high levels of interleukin lbeta, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interleukin-1 beta; IL-1B; human; polymorphism; inflammation; coronary artery disease; osteoporosis; nephropathy; alopeda areata; Graves disease; systemic lupus erythematosus; lichen sclerosis; ulcerative colitis; diabetic retinopathy; periodontal disease; juvenile chronic arthitis; psoriasis; insulin dependent diabetes; asthma; lung fibrosis; chronic inflammatory liver disease; rheumatorid arthitis; chronic inflammatory lung disease; antiinflammacory; osteopathic; dermatological; immunosuppressive; antidiabetic; antithyroid; antiarthritis; attirheumatic; antiasthmatic; antithyroid; hepatotropic; antiulcer; diagnosis; therapy; ds.
                            121 AAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATTATTAAATGGGAATATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "IL-1B allele 1 (+6912)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human interleukin-1 beta allele 1 (+6912).
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replace(8904,G)
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                                                                                                                                                                                                                                                                                                      AAA50174 standard; DNA; 9721 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                              8890 AAATGAGCAAATAT 8903
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                                                                                                                             181 AAATGAGCAAATAT 194
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                                                                                                                                                                                                                                                                                                                                                                                                      07-NOV-2000
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Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergy; activated construction; inhibitor; antiinflammatory; antiallergic; antiallasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; oystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8770 GCCIAGITITIAAIAGCIAIGGAAICAAIICAAIIIGGACIGGIGIGCICCICITIAAAIC 8829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8710 TITTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAAAGA 8769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCTAGITITIAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTTTTAAATC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
osteoporosis, nephropathy in diabetes mellitus, alopecia areata, Graves disease, systemic lupus erythematosus, lichen sclerosis, ulcerative colitis, diabetic retinopathy, periodontal disease, juvenile chronic arthritis, psoriasis, insulin dependent diabetes, asthma, chronic inflammatory liver disease, chronic inflammatory lung disease, lung fibrosis, and rheumatoid arthritis (claimed). Identification of the IL-IB allele 2 (+6912) and its involvement in IL-IB overproduction also eables screening assays for identifying IL-IB antagonists that can be used to treat conditions associated with IL-IB allele 2 (+6912). Transgenic animals are also claimed, and can be used to identify IL-IB agonists and antagonists, or to confirm the safety and efficacy of candidate therapeutics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TITTGATICATIGGICTAATITATICAAAGGGGGCAAGAAGTAGCAGIGTCTGTAAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 9721;
                                                                                                                                                                                                                                                                                                                                              Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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Determining whether a subject has or is predisposed to disease associated with IL-1 polymorphism involves determining presence marker or allele comprising IL-1 inflammatory haplotype

Disclosure; Fig 4; 84pp; English.

Di Giovine FS;

Camp NJ,

Duff GW,

WPI; 2001-102903/11. Cox A,

(INTE-) INTERLEUKIN GENETICS INC

99US-0345217.

30-JUN-1999;

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IL-1; interleukin; inflammation; infection; ds.
                                                                                                                                                                                                                                   AAF27666 standard; DNA; 9721 BP
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                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                          Best Local Similarity 100.
Matches 194; Conservative
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                                                                                                                                                                                                       181 AAATGAGCAAATAT 194
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                                                                                                                                                                                                                                                                            Unidentified
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                                                                                                                                                                                                                                                            IL-1B DNA
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The present invention describes a new composition comprising an anticanse oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antinflammatory, antiallergic, antisathmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects affiliat the lungs of a subject. They can be used for treating effects affiliat the lungs of a subject. They can be used for treating effects affiliat the lungs of a subject. They can be used for treating effects affiliate the lungs of a subject. They can be used for treating effects affiliate the lungs of a subject. They can be used for treating esthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including the own reduces side effects. The reduction of the adenosine content of the own reduces side effects. The Acontaining ONS break down with the release of decoxyadenosine which activates adenosine receptors causing and inflammation. AAA33312 to AAA33312, represent the mind of the adenosine repeace the adenosine content the mind of the adenosine receptors causing and inflammation.
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bronchitis, emphysema, respiratory distress syndrome, ischemia or
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                                                                                                                                                                                                     Disclosure; Page 673-675; 1343pp; English
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The present invention relates to a new method for determining whether a subject has or is predisposed to developing a disease or condition that is associated with an IL (interleukin)-1 inflammatory haplotype, comprises detecting at least one allele of the haplotype, where the presence of the allele indicates that the subject is predisposed to the method is useful for determining whether a subject has or is predisposed to inflammatory disease, a degenerative disease, an immunological disorder, an infectious disease, trauma induced disease, or cancer. The above conditions associated with an IL-1 inflammatory that compensates for a causative mutation that is in linkage diseapled disease.
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interleukin-1 receptor antagonist; vasotropic; antiinflammatory;
hypotensive, anticoagulant; antilipaemic; arterial restenosis;
restenosis associated allele; RAA; occlusive cardiovascular disorder;
restenosis detection, ds.
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Pred. No. 1.3e-85;
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82.2%; Score 194; DB
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 194; Conservative 0; Mismatches
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100.0%; Pred. No. 1.3e-85;
ive 0; Mismatches 0; Indels 0.
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WO200071753-A2.

30-NOV-2000

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Gaps 9

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Low adenosine antisense oligonucleotide, phosphorothioate, allergy, human, airway disorder; bronchoconstriction, lung inflammation, surfactant depletion; respiratory, bronchodilator; antinflammatory; immunosuppressive, antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Evaluating risk of unexplained recurrent pregnancy loss in a subject, by testing presence of a variant in interleukin-1 beta promoter region and/or in CD46 gene intron 1 region in a sample obtained from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8710 rititgartóattágróttáatriaattóaaagágagaaagaágrágaagtagtataaaaga 8769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for evaluating and treating risk of unexplained recurrent pregnancy loss (URPL) in a subject suspected of having immunologic reproductive failure. The method involves testing a sample obtained from the subject for the presence of a variant in the human interleukin-lbeta (IL-lbeta) promoter region, and/or a variant in the CD46 gens inron I region, where the presence of the variant indicates an elevated risk of developing recurrent pregnancy loss. The present sequence is human prointerleukin-1 beta (IL-1 beta) gene.
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                                                                                                                                                                                                                                                                                               Hill JA, Wang ZC, Anderson DJ, Yunis EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2 and 3; Page 51-54; 57pp; English.
                                                                                                                                                                                (BGHM ) BRIGHAM & WOMENS HOSPITAL IN
(DAND ) DANA FARBER CANCER INST INC.
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                                       12-SEP-2001; 2001WO-US28465
                                                                                                          12-SEP-2000; 2000US-231785P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is given in a specification relating to a method for determining whether a subject has or is predisposed to developing an arterial restenosis. The method comprises detecting a restenosis associated allele (RAA) in a nucleic acid sample from the subject, where detection of the RAA indicates that the subject has or is predisposed to the development of a restenosis. The restenosis associated allelic diagnosis of occlusive cardiovascular disorder. The diagnosis allows the most suitable treatment methods for restenosis to be used e.g. selecting therapies for initial vascular stenosis most likely the available to avoid subsequent stenoses. The detection methods identify restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unexplained recurrent pregnancy loss; immunologic reproductive failure; URPL; prointerleukin-lbeta; IL-lbeta; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapeutics, agonists and antagonists, (proteins, peptides, peptidomimetics, small molecules or nucleic acids, e.g. anti-sense, ribozyme and triplex nucleic acids) which are used to treat restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8710 TTTTGATTCATTGGTCTAATTTATTCAAAGGGGGAAGAAGTAGCAGTGTCTGTAAAAGA 8769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8770 GCCTAGITITIAATAGCTAIGGAATCAATITGAATITGGACTGGTGTGTCTCTTTAAATC 8829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing or determining susceptibility to developing restenosis involves detecting restenosis associated allele in a nucleic acid
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                                                                                                                                                                                                                                                                                                   Stephenson K;
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Pred. No. 1.3e-85;
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                                                                                                                                                                                                                        (INTE-) INTERLEUKIN GENETICS INC
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Best Local Similarity 100.
Matches 194; Conservative
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01-NOV-1999;
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24-MAR-2000; 2000WO-US08020. (UYEC-) UNIV EAST CAROLINA. WO200062736-A2. 06-APR-1999; 26-OCT-2000

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -

Disclosure; Page 221-227; 1592pp; English

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense cligonucleotides the A is replaced by a 'universal' or alternative base. (I) can have respiratory, bronchodilator, antinflammatory, analgesic, immunosuppressive, antisathmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, contral nervous system (CNS) and peripheral nervous and non-nervous system peptide receptors, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (specially pulmonary obstruction and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasociated with a disease of condition selected from pulmonary vasociated with a disease (CDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary transplantation rejection, pulmonary inflammation, emphysema, chronic obstruction, pulmonary distress syndrome the and antisense oligonucleotides used in the exemplification of the present invention. the present invention.

Seguence 29433 BP; 8714 A; 6519 C; 5920 G; 8278 T; 2 other;

ö 0; Gaps Query Match
Best Local Similarity 100.0
Matches 194; Conservative

TITIGATICALIGGICIAATITATICAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA 60 Пр 8

22237 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTTTTAAATC 22296 61 GCCTAGTTTTTAATAGCTATGGAATCAATTTGGACTGGTGTGCTCTTTAAATC 120 g ò

22297 AAGTCCTTTAATTAAGACTGAAAATATATATAGCTCAGATTATTTAAATGGGAATATTTAT 22356 121 AAGICCTITAATTAAGACTGAAAATATATATAAGCTCAGATTATTTAAATGGGAATATTTAT 180 ò

22357 AAATGAGCAAATAT 22370

82.2%; Score 194; DB 21; Length 29433; 100.0%; Pred. No. 1.2e-85; tive 0; Mismatches 0; Indels 0;

AAATGAGCAAATAT 194 181

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AA923615 ng98b03.s
W38319 zc77b02.s1
AA131744 z135f02.s
A1022364 ow64g05.x
A1678441 tu82d01.x
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Copyright (c) 1993 - 2003 Compugen Ltd.
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	ALIGNN 324 k iol Homo INTERLEUH in thordata; rimates; rimates; rute, Car tute, Car isberg, Ph nih.gov nih.gov nih.gov nih.gov nih.gov nih.gov nih.gov nih.gov nih.gov nih.gov nih.gov nih.gov nih.gov nih.gov nih.gov nih.gov
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000000000 000 0 000 0 0 0 0 0 0 0 0 0	RESULT 1 AA923615/C LOCUS DEFINITION ACCESSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT

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/organism="Homo sapiens"
Seq primer: mob.REGA+ET
High quality sequence stop: 368.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 413)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dubwque,T., Favello,A., Glash,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,N., Mardis,E.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
Underwood,K., Woldmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 ATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GITITIAAIAGCIAIGGAAICAAIICAAIIIGGACIGGIGGIGCICICIIIAAAICAAGIC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 GITITIAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGTCTCTTTTAAATCAAGTC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITTAATTAAGACTGAAAATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTTAATTAAGACTGAAAATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 ATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.1%; Score 189; DB 9; Length 324; ilarity 100.0%; Pred. No. 7e-93; Conservative 0; Mismatches 0; Indels
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 214.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 AGCAAATAT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCAAATAT 39
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W38319/c
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JOURNAL
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                                         FEATURES
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/db_xref="Homo.1262503"
/db_xref="taxon:9606"
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Tan, F., Trevaskis, E., Waterston, T., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, K., Williamson, A., Wohldmann, P. and Wilson, R., Washington University School of Medicine

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810
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2135f02.81 Soares pregnant_uterus NbHPU Homo sapiens cDNA clone
AMAGE:503931 3' similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
INAGE Consortium (info@inage.llnl.gov) for further information.
Seg primer: -40M13 Evd. from Amersham
High quality sequence stop: 277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 GTTTTTAATAGCTATGGAATCAATTTCAATTTGGACTGGTGTGCTCTCTTTAAATCAAGTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 ATTCATTGGTCTAATTTATTCAAAGGGGCAAGAAGTAGCAGTGGTCTGTAAAAGAGCCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GITITIAATAGCTAIGGAAICAATICAATITIGGACIGGIGIGCICTCTITIAAATCAAGIC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTTAATTAAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 80.1%; Score 189; DB 14; Length 413; Best Local Similarity 100.0%; Pred. No. 7.2e-93; Matches 189; Conservative 0; Mismatches 0; Indels (
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521 bp mRNA linear EST 28-AUG-1998 clone IMAGE: 1651640 3' similar to gb: M15330 INTERLEUKIN-1 BETA A1022364
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 521)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This Concortium (linfc@image.llnl.gov) for further information.
Insert Length: 1077 Std Error: 0.00
Seq primer: -40ml3 fwd. Err from Amersham
High quality sequence stop: 403.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 ATTCATTGGTCTAATTTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCTTA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GITITITAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTCTTTAAATCAAGTC 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="Scares senescent fibroblasts_NbHSF"
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                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                              Length 514;
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100.0%; Pred. No. 7.4e-93;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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AI022364.1 GI:3237605
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100. Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 AGCAAATAT 194
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1763 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI678441 EST 15-DEC-1999 tu82d01.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2257537 3' similar to gb:MI5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                 ö
                             RI
                                                                                    Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bamaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 528)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL CANDER INStitute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)
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/clone lib="nrXGE:25A5 Gas4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTITAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTTAAATG 185
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: E; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5,
                                                                                                                                                                                                                                                                                                                                                                                              172 GITITITAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGTCTCTTTAAATCAAGTC 113
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GITITIAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTCTTTAAATCAAGTC
                                                                                                                                                                                                                                                                                         80.1%; Score 189; DB 9; Length 521; 100.0%; Pred. No. 7.4e-93;
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High quality sequence stop: 404.
Location/Qualifiers
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Best Local Similarity 100.
Matches 189; Conservative
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A1678441/c
LOCUS
DEFINITION
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/clone_lib="NCI_CGAP_C09"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AGCAAATAT 54
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                                                                                                                                                                                                                                                                                                                                                                                    Matches 189;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.B. Consortium/LLML at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 221-272, STAAA)n#Simple_repeat
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UI-H-DHO-auo-f-03-0-UI.81 NCI_CGAP_DHO Homo sapiens CDNA clone HAGE:5872130 3', mRNA sequence.
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Jab host="DHIOB (Life Technologies)"

/note="Organ: Lung; Vector: pT70--Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; modified polylinker; Site 1: EcoR I; Site 2: Not I; VI CGAP DHO is a cDNA library containing the following tissue(s); VS-8 Cell line from Metastatic Chondrosarcoma in Lung The library was constructed according to Bonaldo,
signet ring cell features"
/lab host="DH10B"
/note="Crgan: stomach, Vector: pCNV-SPORT6; Site 1: Sall; Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. (base 1 to 548)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                     227 ATTCATTGGTCTAATTTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTA 168
                                                                                                                                                                                                                                                                                                                                                                                  GTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTTTAAATCAAGTC 125
                                                                                                                                                                                                                                                                                                                                                                                                            167 GTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTTTTAAATCAAGTC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 CITTAATTAAGACTGAAAATATATAAGCTCAGATTATTTAAATGGGAATATTTAAATG 185
                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                           6 ATTCATTGGTCTAATTTATTCAAAGGGGCCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTA 65
                                                                                                                                                                                                    Length 528;
                                                                                                                                        1 others
                                                                                                                                                                                                                                               0; Indels
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/db_xref="taxon:9606"
/db_xref=staxon:9606"
/clone=lib="NGI GAP DHO"
/tissue_type="Metastatic Chondrosarcoma"
                                                                                                                                                                                                  80.1%; Score 189; DB 9; L
100.0%; Pred. No. 7.4e-93;
iive 0; Mismatches 0;
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                                                                                                                11549-011"
                                                                                                                                   98 C.
                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 189; Conservative
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Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into PTT3-Pac vector. The oligoniclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTGC.

TAG_LIB=UI.H-DHO
TAG_TISSUEL-IUNG
TAG_SEQ=AGATCATTGC.

TAG_SEQ=AGATCATTGC.

7.2 a 95 c 123 g 158 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1351 Std Srror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 414.
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Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. (bases 1 to 554)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 ATTCATTGGTCTAATTTTTCAAAGGGGGCAAGAAGTAGCAGTGCTGTGTAAAAGGGCCTA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GITITIAATAGCIATGGAATCAATTCAATTTGGACTGGTGTGCTCTCTTTAAATCAAGTC 125
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100.0%; Pred. No. 7.5e-93;
iive 0; Mismatches 0;
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Similarity
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: capbs-romail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                  /note==Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from REAF colon tumor, and was then primed with a Not I coligo (dT) primer: Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (Soares4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW273081 CGAP CO14 Homo sapiens cDNA clone IMAGE:2801425 3' similar to gb:MI5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mENA
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1 (bases 1 to 618)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 GITITITAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGTCTCTTTAAATCAAGTC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 GTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCCTCTTTAAATCAAGTC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 CITIAATITAAGACIGAAATATATATAAGCICAGATIATITAAAAIGGGAATATITATAAAIG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                  231 ATTCATTGGTCTAATTTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCTA 172
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0
                                                                                                                                                                                                                                                                                               80.1%; Score 189; DB 9; Length 554; 100.0%; Pred. No. 7.5e-93; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                         1 others
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Location/Qualifiers
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
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/clone="IMAGE:2801425"
/clone_lib="NCI_CGAP_CO14"
                                                                                                                                                                                                                                         126 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW273081
AW273081.1 GI:6660111
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                                                                                                                                                                                                                                                                                                                                                    Conservative
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NGT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)
Conteat: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA FORWARD

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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; Pred. No. 7.6e-93;
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according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated come ECR I adaptor, digested with Not I, and cloned directionally into pT773-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATGC.
TAG LIBSUT-lung
TAG LIBSUT-lung
TAG LISSUE-lung
TAG SEQ-AGATCATTCC.
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/note="Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR i; Site 2: Not I; NOT (CAP_FSI is a CDNA library Containing the following tissue[6]: Fibrosarcoma Cell line HT-1088 (ATCC number CCL-121). The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the CMT3-Pac vector and contains a library tag sequence that is located between the Not I site and the CMT3-Fac vector tag for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chong Heov
Gutkind, Ph.D., Myung Hee Park, Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Preparation: Stratagene, Inc.
CDNA General Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
Www-bio.llnl.gov/bbr/jmage/image.html
Insert Length: 1651 Std Error: 0.00
                                        CGAP_Fs1 is
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Eukaryota, Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 817)
NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
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100.0%; Pred. No. 7.8e-93;
iive 0; Mismatches 0;
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AI609005.1 GI:4618172
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Best Local Similarity
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TITLE
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source

FEATURES

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Email: cgapbs-romail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Mashington University Genome Sequencing Center

Clone distribution: NGI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1104 Std Error: 0.00

High quality sequence stop: 409

POLYA-NO.
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone lib="Athersys RAGE Library"
/cell_line="H1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression
/Nature Biotechnology, in press. Note that even though the
cell type indicated is H1080, since a random activation
method was used, these sequence tags are not necessarily
method was used, these sequence tags are not necessarily
a 184 c 219 g 254 t
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone="IMAGE:213907"
/clone lib="NCI CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
                                                                                                                                                                                                                                                                                                                    DB 12; Length 911;
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100.0%; Pred. No. be.
... 0; Mismatches

    .549
    /organism="Homo sapiens"

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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                        SETIANA linear EST 21-APR-2001 RESTIANA LINEAR EST 21-APR-2001 RESTIANA Athersys RAGE Library Homo sapiens CDNA, mRNA sequence. BG194765
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Harrington, J. Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,
Harrington, J. Sherf, B., Rundlett, S., Jackson, P. D., Whittington, J. Grain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,
Lerner, L., Costanzo, D., McBligott, K., Boozer, S., Mays, R., Smith, Jerner, L., Costanzo, D., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M. Hess, J., Cothren, K., Lo, K., Offenbacher Creation of genome-wide protein expression libraries using random naturation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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3201 Carnegle Ave, Cleveland, OH 44115, USA
Tel: 216 431 9956
Fax: 216 361 9596
Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.1%; Score 189; DB 9; I
100.0%; Pred. No. 7.9e-93;
ive 0; Mismatches 0;
                                                             'organism="Homo sapiens"
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Location/Qualifiers
            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 189; Conservative
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DEFINITION ACCESSION

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RESULT 12 BG194765/c

SOURCE ORGANISM

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                                  Gev stage="adult"

[lab_host="DH10B (phage-resistant)"

[hote="Organ: lung, Vector: pT773D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIS19707 746 bp mRNA linear EST 29-AUG-2001
603061928T1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211294 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mamala, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (base 1 to 746)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
differentiated (4 pooled tumors, including primary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1530 row: g column: 07
High quality sequence start: 3
High quality sequence stop: 740.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 TGTCTGTAAAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTG 127
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                                                                                                                                                                                                                                                                                    1 others
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/clone="ITMAGE:5211294"
/clone_lib="NIH_MGC_118"
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/lab_host="DH10B"
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TITLE
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UI-H-DP0-avf-1-11-0-UI.s1 NCI_CGAP_FS1 Homo sapiens cDNA clone
UNAGE:5878810 3', mRNA sequence.
cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library."
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Tissue Procurement: Dr. Mary Hendrix
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LiNL at: http://image.lnl.gov
The following repetitive elements were found in this CDNA
Seq primer: MI3 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 793)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                     66 GITITITAATAGCTATGGAATCAATTTGGACTGGTGTGCTCTCTTAAATCAAGTC 125
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                                                                                                                                                                                                                                                                                                       148 ATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTA 89
                                                                                                                                                                                                                                                                                                                                                                                               88 GTTTTTAATAGCTATGGAATCAATTGAATTTGGACTGGTGTGCTCTTTAAATCAAGTC 29
                                                                                                                                                                                                                                                                            6 ATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTA
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Pred. No. 9.5e-70;
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100.0%; Pred. No. »...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 CITTAATTAAGACTGAAAATATATAAG 152
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BM999417.1 GI:19724318
                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 147; Conservative
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Unpublished (1997)
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Search completed: March 17, 2003, 21:29:38 Job time : 1464 secs